

STIC-Biotech/ChemLib

116700

From: Schnizer, Holly  
Sent: Thursday, December 18, 2003 9:53 AM  
To: STIC-Biotech/ChemLib  
Subject: 09/185,904

Please search all databases (inc. interference) for SEQ ID NO:33.

Thank you.

Holly Schnizer  
AU 1653  
CM1-9E09  
305-3722  
mailbox: CM1-9B01

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 12/18/03  
Date Completed: 12/19/03  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: OSP  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 18, 2003, 17:07:54 ; Search time 17 Seconds

(without alignments)  
824.350 Million cell updates/sec

Title: US-09-185-904A-33

Perfect score: 1543  
Sequence: 1 MTEQALSPKDFLAGIAA.....LRMGAFVLVYDELKVI 298

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1543	100.0	298	1 ADT3_HUMAN	P12236 homo sapien
2	1512	98.0	298	1 ADT3_BOVIN	P32007 bos taurus
3	1463	94.8	298	1 ADT2_HUMAN	P08141 homo sapien
4	1451	94.0	298	1 ADT2_RAT	P08073 ratu norv
5	1445	93.6	298	1 ADT2_MOUSE	P51881 mus musculu
6	1424	92.3	298	1 ADT1_RAT	P05962 ratu norv
7	1418	91.9	298	1 ADT1_MOUSE	P48962 bos taurus
8	1417	91.8	297	1 ADT1_BOVIN	P02722 bos taurus
9	1409	91.3	298	1 ADT1_HUMAN	P12235 homo sapien
10	1254.5	81.3	299	1 ADT1_MOUSE	P02723 ratu norv
11	1204	78.0	301	1 ADT1_MOUSE	P02723 ratu norv
12	978	63.4	339	1 ADT1_MOUSE	P02723 ratu norv
13	778.5	50.5	307	1 ADT3_YEAST	P18238 saccharomyc
14	772	50.0	308	1 ADT1_CHICK	P27080 chlamydomon
15	769	49.8	322	1 ADT1_MOUSE	P02722 bos taurus
16	768	49.8	386	1 ADT1_MOUSE	P02722 bos taurus
17	766	49.6	313	1 ADT1_MOUSE	P02722 bos taurus
18	765	49.4	305	1 ADT1_MOUSE	P02722 bos taurus
19	760.5	49.3	318	1 ADT2_YEAST	P18238 saccharomyc
20	750.5	48.6	385	1 ADT2_ARATH	P40941 arabidopsi
21	750	48.6	387	1 ADT1_MOUSE	P02722 bos taurus
22	748	48.5	386	1 ADT1_MOUSE	P02722 bos taurus
23	747	48.4	382	1 ADT1_MOUSE	P02722 bos taurus
24	744	48.2	387	1 ADT2_MOUSE	P51881 mus musculu
25	742.5	48.1	381	1 ADT1_MOUSE	P02722 bos taurus
26	740	48.0	331	1 ADT1_MOUSE	P02722 bos taurus
27	739.5	47.9	309	1 ADT1_MOUSE	P02722 bos taurus
28	737.5	47.8	309	1 ADT1_MOUSE	P02722 bos taurus
29	727	47.1	331	1 ADT2_MOUSE	P51881 mus musculu
30	305.5	19.8	565	1 CMC2_MOUSE	P02722 bos taurus
31	302	19.6	588	1 CMC2_MOUSE	P02722 bos taurus
32	300	19.4	330	1 GPC_BOVIN	P02722 bos taurus
33	299	19.4	307	1 ODC2_YEAST	P02722 bos taurus

34	295	19.1	678	1 CMCI_HUMAN	O75746 homo sapien
35	289.5	18.8	322	1 GPC_RAT	P16261 ratu norv
36	287.5	18.6	702	1 CMCI_MOUSE	O21153 caenorhabdi
37	286	18.5	325	1 UCP5_HUMAN	O95258 homo sapien
38	285	18.5	332	1 GPC_HUMAN	P16260 homo sapien
39	284	18.4	325	1 UCP5_MOUSE	O94282 mus musculu
40	282.5	18.3	326	1 YE08_SCHPO	O13805 schizosacch
41	280	18.1	675	1 CMCI_HUMAN	O94280 homo sapien
42	272	17.6	315	1 MFT_HUMAN	O94281 homo sapien
43	270	17.5	315	1 SAI8_HUMAN	O94282 homo sapien
44	265	17.2	312	1 UCP3_HUMAN	P55916 homo sapien
45	265	17.2	676	1 CMCI_MOUSE	O94283 mus musculu

## ALIGNMENTS

RESULT 1  
ADT3\_HUMAN STANDARD; PRT; 298 AA.  
AC P12236; 096C49;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE ADP/ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)  
DE (adenine nucleotide translocator 3) (ANT 3).  
CN SLC25A6 OR ANT3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89236396; PubMed=2541251;  
RA Cozens A.L., Runswick M.J., Walker J.E.;  
RT "DNA sequences of two expressed nuclear genes for human mitochondrial  
ADP/ATP translocase.";  
RL 1 Mol Biol 206:261-280(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Zhou J., Yu W., Tang H., Tsang Y.T.M., Bouck J., Gibbs R.A.,  
RA Margolin J.F.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain, Cervix, Eye, and Lung;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,  
RA Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueding T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Bork S.S., Lequellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,  
RA Bork S.S., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Vailation D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Faley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Buterfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,  
RA Scherch A., Schein J.B., Jones S.J.M., Maira M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [4]  
RP SEQUENCE OF 36-298 FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=88124845; PubMed=2829183;  
RA Houldsworth J., Altardi G.;  
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA

RT level in adult human liver." ;  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381 (1988).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----  
 DR EMBL; J03592; AAA6750.1; -;  
 DR EMBL; AY007135; AAG01998.1; -;  
 DR EMBL; BC007285; AAH07285.1; -;  
 DR EMBL; BC007850; AAH07850.1; -;  
 DR EMBL; BC008737; AAH08737.1; -;  
 DR EMBL; BC008935; AAH08935.1; -;  
 DR EMBL; BC014775; AAH14775.1; -;  
 DR PIR; S03894; S03894.  
 DR Genew; HGNC:10992; SLC25A6.  
 DR MIM; 300151; -;  
 DR MIM; 403000; -;  
 DR GO; GO:0005744; C:mitochondrial inner membrane translocase co. .; TAS.  
 DR GO; GO:0005471; F:ATP/ADP antiporter activity; NAS.  
 DR GO; GO:0006854; P:ATP/ADP exchange; TAS.  
 DR InterPro; IPR002067; Mit\_carrier.  
 DR InterPro; IPR002030; Mit\_uncoupling.  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR Pfam; PF00153; mito\_carr; 3.  
 DR PRINTS; PRO0926; MITOCARRIER.  
 DR PRINTS; PRO0784; MTUNCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KW Multigene family.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 100 1.  
 FT REPEAT 101 208 2.  
 FT REPEAT 209 298 3.  
 FT CONFLICT 105 298 S -> F (IN REF. 3; AAH14775).  
 FT CONFLICT 242 242 S -> F (IN REF. 3; AAH14775).  
 FT SEQUENCE 298 AA; 32866 MW; 18534E9F0E49672F CRC64;  
 Query Match 100.0%; Score 1543; DB 1; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 3; DE-128;  
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MTEOAI SFADFLAGIAAIAISKTA VAPIERVKLLIQVHASQIAADKQYKGI VDCIVR 60  
 DB 1 MTEOAI SFADFLAGIAAIAISKTA VAPIERVKLLIQVHASQIAADKQYKGI VDCIVR 60  
 QY 1 IPKEQGLT FWRKGLAVIYFPFOALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLSG 120  
 DB 1 IPKEQGLT FWRKGLAVIYFPFOALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLSG 120  
 QY 121 GAAGATSLICVYPLDFAFTRILADVSGSGTERBERFGDCCVKTGSDGIRGLYQGSVS 180  
 DB 121 GAAGATSLICVYPLDFAFTRILADVSGSGTERBERFGDCCVKTGSDGIRGLYQGSVS 180  
 QY 181 VGGIIYRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQTVAAGVVSYPFDIVRRMM 240  
 DB 181 VGGIIYRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQTVAAGVVSYPFDIVRRMM 240

QY 241 QSGRKGADIMYTGTVDCWRKIPDEGGKAFPKGAMSVNLKMGGAFLVLYDELKKVI 298  
 DB 241 QSGRKGADIMYTGTVDCWRKIPDEGGKAFPKGAMSVNLKMGGAFLVLYDELKKVI 298  
 RESULT 2  
 ADT3\_BOVIN STANDARD; PRT; 298 AA.  
 AC P32067;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE ADP/ATP carrier protein, isoform T2 (ADP/ATP translocase 3) (Adenine  
 DE nucleotide translocator 3) (ANT 3).  
 GN SLC25A6 OR ANT3.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89229093; Pubmed=2540808;  
 RA Powell S.J., Medd S.M., Runswick M.J., Walker J.B.;  
 RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed  
 RT differences in various tissues." ;  
 RL Biochemistry 28:866-873 (1989).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----  
 DR EMBL; M24103; AAA30769.1; -;  
 DR PIR; B43646; B43646.  
 DR InterPro; IPR002067; Mit\_carrier.  
 DR InterPro; IPR002030; Mit\_uncoupling.  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR Pfam; PF00153; mito\_carr; 3.  
 DR PRINTS; PRO0926; MITOCARRIER.  
 DR PRINTS; PRO0784; MTUNCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KW Multigene family.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 111 1.  
 FT REPEAT 112 208 2.  
 FT REPEAT 209 298 3.  
 FT SEQUENCE 298 AA; 32877 MW; 1C34E7DF6EDE4061 CRC64;  
 Query Match 98.0%; Score 1512; DB 1; Length 298;  
 Best Local Similarity 97.7%; Pred. No. 1; 9e-125;  
 Matches 291; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MTEOAI SFADFLAGIAAIAISKTA VAPIERVKLLIQVHASQIAADKQYKGI VDCIVR 60  
 DB 1 MTEOAI SFADFLAGIAAIAISKTA VAPIERVKLLIQVHASQIAADKQYKGI VDCIVR 60

QY 61 IPKEGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120  
 DB 61 IPKEGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDPFARTRLADVKGSGTEREFGDGLVTKYSDGIRGLYOGFSVS 180  
 DB 121 GAAGATSLCFVYPLDPFARTRLADVKGSGTEREFGDGLVTKYSDGIRGLYOGFSVS 180  
 QY 181 VGGIITRAAYFGVYDPAKGMPPDKNTHIVSMIAQTVAAGVSYSPDTPARRMM 240  
 DB 181 VGGIITRAAYFGVYDPAKGMPPDKNTHIVSMIAQTVAAGVSYSPDTPARRMM 240  
 QY 241 QSGRKGADIMYTGTLDCWRKIFRDEGKAFPKGAMSNVLRGMGAFVLYLDELKVI 298  
 DB 241 QSGRKGADIMYTGTLDCWRKIFRDEGKAFPKGAMSNVLRGMGAFVLYLDELKVI 298

RESULT 3  
 ADT2 HUMAN STANDARD; PRT; 298 AA.  
 ID ADT2 HUMAN STANDARD; PRT; 298 AA.  
 AC P05141; 043350;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE ADP carrier protein, fibroblast isoform (ADP/ATP translocase 2)  
 GN (Adenine nucleotide translocator 2) (ANT 2).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=90375457; PubMed=2168878;  
 RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Basesga R., Murrel J.;  
 RT "The human fibroblast adenine nucleotide translocator gene. Molecular  
 cloning and sequence.";  
 RL J. Biol. Chem. 265:16060-16063(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87166056; PubMed=3031073;  
 RA Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,  
 RA Basesga R.;  
 RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is  
 growth-regulated.";  
 RL J. Biol. Chem. 262:4355-4358(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Chen C.N., Su Y., Baybayan P., Siruno A., Nagaraja R.,  
 RA Mazarella R.A., Schlessinger D., Chen E.Y.;  
 RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Becker M., Graves T., Ozersky P.;  
 RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 47-298 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=88124845; PubMed=2829183;  
 RA Houldsworth J., Altardi G.;  
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA  
 level in adult human liver.";  
 RL Pric. Natl. Acad. Sci. U.S.A. 85:377-381(1988).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; M57424; AAA51737.1; -;  
 DR EMBL; J02683; AAA35579.1; -;  
 DR EMBL; L78810; AAB39266.1; -;  
 DR EMBL; AC004000; AAB96347.1; -;  
 DR EMBL; J03591; AAA6749.1; -;  
 DR PIR; A29132; A29132.  
 DR Gene; HGNC:10991; SLC25A5.  
 DR MIM; 300150;  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0015207; F:adenine transporter activity; TAS.  
 DR GO; GO:0006832; P:small molecule transport; TAS.  
 DR InterPro; IPR002067; Mit\_carrier.  
 DR InterPro; IPR001993; Mit\_uncoupling.  
 DR InterPro; IPR001993; Mit\_carrier.  
 DR Pfam; PF00153; mito\_carr; 3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUNCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KW Multigene family.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 111 1.  
 FT REPEAT 112 208 2.  
 FT REPEAT 209 298 3.  
 FT CONFLICT 6 6 V -> L (IN REF. 2).  
 FT CONFLICT 111 66 G -> E (IN REF. 2).  
 FT CONFLICT 162 111 R -> L (IN REF. 4 AND 5).  
 FT CONFLICT 162 162 V -> G (IN REF. 5).  
 SQ SEQUENCE 298 AA; 32895 MM; F973G3ARD92C49D3 CRC64;  
 Query Match 94.8%; Score 1463; DB 1; Length 298;  
 Best Local Similarity 92.9%; Pred. No. 3.8e-121;  
 Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 MTEQAIIFADPLAGIAAIAISKTAVPIERVKLLLOVQASKQIADKQYKGIYDCIVR 60  
 DB 1 MTEQAIIFADPLAGIAAIAISKTAVPIERVKLLLOVQASKQIADKQYKGIYDCIVR 60  
 QY 61 IPKEGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120  
 DB 61 IPKEGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDPFARTRLADVKGSGTEREFGDGLVTKYSDGIRGLYOGFSVS 180  
 DB 121 GAAGATSLCFVYPLDPFARTRLADVKGSGTEREFGDGLVTKYSDGIRGLYOGFSVS 180  
 QY 181 VGGIITRAAYFGVYDPAKGMPPDKNTHIVSMIAQTVAAGVSYSPDTPARRMM 240  
 DB 181 VGGIITRAAYFGVYDPAKGMPPDKNTHIVSMIAQTVAAGVSYSPDTPARRMM 240  
 QY 241 QSGRKGADIMYTGTLDCWRKIFRDEGKAFPKGAMSNVLRGMGAFVLYLDELKVI 296  
 DB 241 QSGRKGADIMYTGTLDCWRKIFRDEGKAFPKGAMSNVLRGMGAFVLYLDELKVI 296

RESULT 4  
 ADT2 RAT STANDARD; PRT; 298 AA.  
 ID ADT2 RAT STANDARD; PRT; 298 AA.  
 AC Q09073;  
 DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)  
 DE (Adenine nucleotide translocator 2) (ANT 2).  
 GN SLC25A5 OR ANT2.  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN  
 RP  
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
 RX MEDLINE=94002161; PubMed=8393900;  
 RA Shinohara Y., Kamada M., Yamazaki N., Terada H.;  
 RT "Isolation and characterization of cDNA clones and a genomic clone  
 RT encoding rat mitochondrial adenine nucleotide translocator.";  
 RL Biochem. Biophys. Acta 1152:192-196(1993).  
 CC  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND  
 CC SKELETAL MUSCLE.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC -----  
 DR EMBL; D12771; BAA02238.1; -;  
 DR InterPro; IPR002067; Mit\_carrier.  
 DR InterPro; IPR002030; Mit\_uncoupling.  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR Pfam; PF00153; mitc\_carr; 3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PROSITE; PR00784; MTUNCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KM Multigene family.  
 KW TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 111 1.  
 FT REPEAT 112 208 2.  
 FT REPEAT 209 298 3.  
 SQ SEQUENCE 298 AA; 32901 MW; 6A59204B987EFB35 CRC64;  
 Query Match 94.0%; Score 1451; DB 1; Length 298;  
 Best Local Similarity 91.9%; Pred. No. 4.3e-120; Indels 0; Gaps 0;  
 Matches 272; Conservative 15; Mismatches 9;  
 QY 1 MTEQAI SPADKFLAGIAIAAISKTA VAPIERVKLLQVHASKOIAADKOYGI VDCIVR 60  
 DB 1 MTDAAVSPADKFLAGIAIAAISKTA VAPIERVKLLQVHASKOITADKOYKGI IDCVR 60  
 QY 61 IPKQGVLSFWRGMLAVIRYFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNIASG 120  
 DB 61 IPKQGVLSFWRGMLAVIRYFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNIASG 120  
 QY 121 GAAGATSLCFYYPIDPAATRLAAVVGSGTFRERFGIDCVTKSGDGRGLVQSGFVS 180  
 DB 121 GAAGATSLCFYYPIDPAATRLAAVVGSGTFRERFGIDCVTKSGDGRGLVQSGFVS 180  
 QY 181 VGGIIIVRAAVFGVYDAKGM LDDPKNTHIVSWMIQTVTA VAVGVVSYPFDIVRRMM 240

DB 181 VGGIIIVRAAVFGVYDAKGM LDDPKNTHIVSWMIQTVTA VAVGVVSYPFDIVRRMM 240  
 QY 241 QSGRKADIVYTCTVQCWRKIFPRDEGKAFFKAMSVLVJGMDGAPFLVLYDELKK 296  
 DB 241 QSGRKADIVYTCTVQCWRKIFPRDEGKAFFKAMSVLVJGMDGAPFLVLYDELKK 296  
 RESULT 5  
 ADT2\_MOUSE STANDARD; PRT; 298 AA.  
 ID ADT2\_MOUSE  
 AC P51881; Q61311;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)  
 DE (Adenine nucleotide translocator 2) (ANT 2).  
 GN SLC25A5 OR ANT2.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN  
 RP  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=97059403; PubMed=8903724;  
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.;  
 RT "Rapid evolution of human pseudautosomal genes and their mouse  
 RT homologs.";  
 RL Mamm. Genome 7:25-30(1996).  
 RN  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skeletal muscle;  
 RA Sheldon J.G.;  
 RL Thesis (1995), University of Cambridge, U.K.  
 RN  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SV;  
 RA Coster P., Laplace C.;  
 RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.  
 RN  
 RN [4]  
 RP REVISIONS.  
 RA Laplace C.;  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 RN  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20432087; PubMed=10974536;  
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;  
 RT "Expression and sequence analysis of the mouse adenine nucleotide  
 RT translocase 1 and 2 genes.";  
 RL Gene 254:57-66(2000).  
 CC  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC -----  
 DR EMBL; U27316; AAC52838.1; -;  
 DR EMBL; U10404; AAA19009.1; -;  
 DR EMBL; X70847; CA550196.1; -;  
 DR EMBL; AF240003; AA64471.1; -;  
 DR MGD; MGI:1353496; SLC25a5.  
 DR InterPro; IPR002067; Mit\_carrier.

DR InterPro; IPR002030; Mit uncoupling.  
 DR InterPro; IPR001993; Mitoch carrier.  
 DR Pfam; PF00153; mito\_carr; 3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUOCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KW Multigene family.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 111 1.  
 FT REPEAT 112 208 2.  
 FT REPEAT 209 298 3.  
 SQ SEQUENCE 298 AA; 32931 MW; 0798E04B987EE20 CRC64;

Query Match 93.6%; Score 1445; DB 1; Length 298;  
 Best Local Similarity 91.6%; Pred. No. 1.4e-119;  
 Matches 271; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTEQAIISPAKDFLAGGIAAISKTAIVPIERVKLLQVQHASKQIADKQYKGIIVDCIVR 60  
 DB 1 MTDAAVSPAKDFLAGGVAIAISKTAIVPIERVKLLQVQHASKQIADKQYKGIIVDCIVR 60  
 QY 61 IPKEGQVSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVGHQTFWRFYFAGNLSAG 120  
 DB 61 IPKEGQVSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVGHQTFWRFYFAGNLSAG 120  
 QY 121 GAAGATSLCFVYPLDFARTRLAADVKGSGTEREFNGLDCLVKITKSDIGRLYQGFVS 180  
 DB 121 GAAGATSLCFVYPLDFARTRLAADVKGSGTEREFNGLDCLVKITKSDIGRLYQGFVS 180  
 QY 181 VGGIITRYAAVFGYVDTAKGMLPDPKNTHTIVSWMIAQTVAAGVSYFPDTRRRMM 240  
 DB 181 VGGIITRYAAVFGYVDTAKGMLPDPKNTHTIFISWIAQSVTAAGLTSYFPDTRRRMM 240  
 QY 241 QSGRGKADIMTGTVDCKRKIFRDEGGAFFKGAWSNVLRMGGAFFVLYVDELKVI 298  
 DB 241 QSGRGKADIMTGTVDCKRKIFRDEGGAFFKGAWSNVLRMGGAFFVLYVDELKVI 298

## RESULT 6

ADT1\_RAT STANDARD; PRT; 298 AA.  
 AC Q05962;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (adenine nucleotide translocator 1) (ANT 1).  
 GN SLC25A4 OR ANT1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_Taxid=10116;  
 RN [1]

RC SEQUENCE FROM N.A.  
 RP STRAIN=Sprague-Dawley, and Wistar; TISSUE=Heart, and Liver;  
 RX MEDLINE=94002161; PubMed=8399300;  
 RA Shirohara Y., Kamida M., Yamazaki N., Terada H.;  
 RT "Isolation and characterization of cDNA clones and a genomic clone encoding rat mitochondrial adenine nucleotide translocator.";  
 RL Biochim. Biophys. Acta 1152:192-196(1993).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.  
 CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER EXTENT, IN BRAIN AND KIDNEY.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----

CC EMBL; X61667; CA943842.1; -;  
 CC EMBL; D12770; BAA02237.1; -;  
 CC PIR; I60173; I60173.  
 DR InterPro; IPR002067; Mit carrier.  
 DR InterPro; IPR002030; Mit uncoupling.  
 DR InterPro; IPR001993; Mitoch carrier.  
 DR Pfam; PF00153; mito\_carr; 3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUOCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KM Multigene family.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 110 1.  
 FT REPEAT 111 208 2.  
 FT REPEAT 209 298 3.  
 SQ SEQUENCE 298 AA; 32989 MW; 66704FF78C6B320 CRC64;

Query Match 92.3%; Score 1424; DB 1; Length 298;  
 Best Local Similarity 89.6%; Pred. No. 1e-117;  
 Matches 267; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQAIISPAKDFLAGGIAAISKTAIVPIERVKLLQVQHASKQIADKQYKGIIVDCIVR 60  
 DB 1 MGDQALSLKDFLAGGIAAISKTAIVPIERVKLLQVQHASKQIADKQYKGIIVDCIVR 60  
 QY 61 IPKEGQVSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVGHQTFWRFYFAGNLSAG 120  
 DB 61 IPKEGQVSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVGHQTFWRFYFAGNLSAG 120  
 QY 121 GAAGATSLCFVYPLDFARTRLAADVKGSGTEREFNGLDCLVKITKSDIGRLYQGFVS 180  
 DB 121 GAAGATSLCFVYPLDFARTRLAADVKGSGTEREFNGLDCLVKITKSDIGRLYQGFVS 180  
 QY 181 VGGIITRYAAVFGYVDTAKGMLPDPKNTHTIVSWMIAQTVAAGVSYFPDTRRRMM 240  
 DB 181 VGGIITRYAAVFGYVDTAKGMLPDPKNTHTIVSWMIAQSVTAAGLTSYFPDTRRRMM 240  
 QY 241 QSGRGKADIMTGTVDCKRKIFRDEGGAFFKGAWSNVLRMGGAFFVLYVDELKVI 298  
 DB 241 QSGRGKADIMTGTVDCKRKIFRDEGGAFFKGAWSNVLRMGGAFFVLYVDELKVI 298

## RESULT 7

ADT1\_MOUSE STANDARD; PRT; 298 AA.  
 AC P48962; G52164;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (adenine nucleotide translocator 1) (AMC1).  
 GN SLC25A4 OR ANT1 OR ANCL.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_Taxid=10090;

```

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=97059403; PubMed=8903724;
RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudautosomal genes and their mouse
  homologs.";
RL Mamm. Genome 7:25-30 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Muscle;
RA Laplace C., Cosset P.;
RL Submitted (SEP-1993) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT "Expression and sequence analysis of the mouse adenine nucleotide
  translocase 1 and 2 genes.";
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
  Altschul S.F., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
  Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
  Brownstein M.J., Umed T.B., Toshyuki S., Carrinci P., Prange C.,
  Rata S.S., Loguailano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
  Bork S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
  Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
  Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
  Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G.,
  Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
  Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
  Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
  human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
  MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
  inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL Outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
  or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U7315; AAC52837.1; -
DR EMBL: X74510; CA52616.1; -
DR EMBL: AF240002; AAF64470.1; -
DR EMBL: BC003791; AAH03791.1; -
DR EMBL: BC026925; AAH26925.1; -
DR PIR: S37210; S37210.
DR MGD: MGI:1353495; S1C25A4.
DR InterPro: IPR002067; Mlt carrier.
DR InterPro: IPR002030; Mlt uncoupling.
DR InterPro: IPR001993; Mitoch carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.

```

```

KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KM Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
FT REPEAT 136 136 F -> L (IN REF. 1).
SQ SEQUENCE 298 AA; 32904 MW; 3A849FEB0981462 CRC64;

Query Match 91.9%; Score 1418; DB 1; Length 298;
Best Local Similarity 88.9%; Pred. No. 3.4e-117;
Matches 265; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

Cy 1 MTEQATSPANDFLAGGIAAISKTAAPVIERVLLQVQHASKOIADKQYKIVDCIVR 60
Db 1 MGQALSFLLDFLAGGIAAASKTAVAPVIERVLLQVQHASKOISAEKQYKGIIDCVR 60

Cy 61 IPKEQVLSFRWGNLANVIRYPTQALNFAFKKQKQIFLGVDKTOFWRYFAGNLASG 120
Db 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKKQKQIFLGVDKTOFWRYFAGNLASG 120

Cy 121 GAAGATSLCVYPLDFARTRLADVKGSGTEREFGDGLVTKTSDDIRGLXQGFSSVS 180
Db 121 GAAGATSLCVYPLDFARTRLADVKGSGTEREFGDGLVTKTSDDIRGLXQGFSSVS 180

Cy 181 VQGIIRYRAAFVGYDTAKMLPDPKNTHTIVSWMTAQTVTAAGVVSYPFDVRRMM 240
Db 181 VQGIIRYRAAFVGYDTAKMLPDPKNTHTIVSWMTAQTVTAAGVVSYPFDVRRMM 240

Cy 241 QSGRKADIVYTGTVDCWKRIFFDEGKAFPKGKMSVTLFGMGAFVLYLYDLKXYI 298
Db 241 QSGRKADIVYTGTVDCWKRIFFDEGKAFPKGKMSVTLFGMGAFVLYLYDLKXYI 298

RESULT 8
ADTI_BOVIN STANDARD; PRT; 297 AA.
ID ADTI_BOVIN
AC P02722;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP,ATP carrier protein, heart isoform T1 (ADP/ATP translocase 1)
DE (Adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovine; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=69229093; PubMed=2540808;
RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
  differences in various tissues.";
RL Biochemistry 28:866-873 (1989).
RN [2]
RP SEQUENCE.
RX MEDLINE=82188267; PubMed=7076130;
RA Aquila H., Mista D., Bultz M., Klingenberg M.;
RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart
  mitochondria.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349 (1982).
RN [3]
RP SEQUENCE OF 207-297 FROM N.A.
RX MEDLINE=66295775; PubMed=3017341;
RA Rasmussen U.B., Wohlrab H.;
RT "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and

```



RT an unusually short 3'-noncoding sequence.";  
 RL Biochem. Biophys. Res. Commun. 138:850-857(1986).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M13783; AAA0363.1; -;  
 DR EMBL; M24102; AAA0768.1; -;  
 DR PIR; A43646; XMBO.  
 DR InterPro; IPR002067; Mit\_carrier.  
 DR InterPro; IPR002030; Mit\_uncoupling.  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR Pfam; PF00153; mito\_catr; 3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MTUNCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KM Multigene family; Methylation.  
 FT INIT\_MET 0  
 FT MOD\_RES 1 1 BLOCKED.  
 FT MOD\_RES 51 51 METHYLATION (POTENTIAL).  
 FT TRANSSEM 11 28 1 (POTENTIAL).  
 FT TRANSSEM 72 90 2 (POTENTIAL).  
 FT TRANSSEM 116 133 3 (POTENTIAL).  
 FT TRANSSEM 175 194 4 (POTENTIAL).  
 FT TRANSSEM 213 230 5 (POTENTIAL).  
 FT TRANSSEM 272 290 6 (POTENTIAL).  
 FT REPEAT 111 110 1.  
 FT REPEAT 207 207 2.  
 FT REPEAT 208 297 3.  
 SQ SEQUENCE 297 AA; 32836 MW; A582D3C4A40EB48 CRC64;  
 Query March 91.8%; Score 1417; DB 1; Length 297;  
 Best Local Similarity 89.2%; Pred. No. 4.1e-117;  
 Matches 265; Conservative 19; Mismatches 13; Indels 0; Gaps 0;  
 QY 2 TEQAIISPAKDFLAGIAAIAISKTAVAPIERVKLLQVQHASKQIAADKQYGIYDCIVRI 61  
 Db 1 SDQALSFIDKPLAGVAIAISKTAVAPIERVKLLQVQHASKQISAEKQYGIITDCIVRI 60  
 QY 62 PKEGVTSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVYDHTQFWRYPAGNLASGG 121  
 Db 61 PKEGGFSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVYDHTQFWRYPAGNLASGG 120  
 QY 122 AAGATSLCFVYPLDPFARTRILADVGKSTEEFEGDGLCVLKTKISGIRGLYOGFSVSU 181  
 Db 121 AAGATSLCFVYPLDPFARTRILADVGKGAQREFTGLNGCTIKRISGIRGLYOGFSVSV 180  
 QY 182 QGIIIVAAVGVYDVTAKGMLPDKNTIIVVSMIAQTVTVAVAGVSPFPTVRRMMQM 241  
 Db 181 QGIIIVAAVGVYDVTAKGMLPDKNTIIVVSMIAQTVTVAVAGVSPFPTVRRMMQM 240  
 QY 242 SGRKADIMVTGVDVCRKIFRDGGAFFKAGANSVLKMGAFVLVLYDELKVI 238  
 Db 241 SGRKADIMVTGVDVCRKIFRDGGAFFKAGANSVLKMGAFVLVLYDEIKFV 237  
 RESULT 9  
 ADTI\_HUMAN  
 ID ADTI\_HUMAN STANDARD; PRT; 298 AA.  
 AC P12235;

DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP  
 DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1).  
 GN SLC25A4 OR ANT1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89235396; PubMed=2541251;  
 RA Cozens A.L., Runswick M.J., Walker J.E.;  
 RT "DNA sequences of two expressed nuclear genes for human mitochondrial  
 RT ADP/ATP translocase.";  
 RL J. Mol. Biol. 206:261-280(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89340499; PubMed=2547778;  
 RA Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,  
 RA Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;  
 RT "A human muscle adenine nucleotide translocator gene has four exons,  
 RT is located on chromosome 4, and is differentially expressed.";  
 RL J. Biol. Chem. 264:13998-14004(1989).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86041149; PubMed=2823266;  
 RA Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;  
 RT "cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack  
 RT of a leader peptide, divergence from a fibroblast translocator cDNA,  
 RT and coevolution with mitochondrial DNA genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22388257; PubMed=1247792;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.A., Hale F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uebli T.B., Toebehyuk S., Carninci P., Prange C.J.,  
 RA Rata S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullany P.H.,  
 RA Bosak S.A., McEwan P.V., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huij S.W.,  
 RA Vallajon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [5]  
 RP SEQUENCE OF 1-37 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=88124845; PubMed=2829183;  
 RA Houldsworth J., Attardi G.;  
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA  
 RT level in adult human liver.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).  
 RN [6]  
 RP VARIANTS PRO PRO-114 AND MET-289.  
 RX MEDLINE=20385067; PubMed=10926541;  
 RA Kaukonen U., Juselius J.K., Tiantti V., Kyttala A., Zeviani M.,  
 RA Comi G.P., Keranen U., Peltonen L., Suomalainen A.;  
 RT "Role of adenine nucleotide translocator 1 in mtDNA maintenance.";  
 RL Science 289:782-785(2000).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE

CC	MITOCHONDRIAL INNER MEMBRANE
CC	-1- SUBUNIT: Homodimer
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC	-1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC	-1- DISEASE: Defects in SLC25A4 are a cause of autosomal dominant progressive external ophthalmoplegia with various mitochondrial DNA deletions (PEO). Patients with PEO have mitochondrial myopathy, progressive external ophthalmoplegia, and other abnormalities associated with multiple different deletions of mitochondrial DNA.
CC	-1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.ebi.ac.uk/announcements">http://www.ebi.ac.uk/announcements</a> or send an email to <a href="mailto:license@ebi.ac.uk">license@ebi.ac.uk</a> ).
CC	-----
DR	EMBL; J02966; AAA61223.1; -
DR	EMBL; J03593; AAA6751.1; -
DR	EMBL; J04982; AAA51736.1; -
DR	EMBL; BC008664; AAH08664.1; -
DR	PIR; A44778; A44778
DR	Genew; HGNC:10990; SLC25A4.
DR	MIM; 157640; -
DR	GO; GO:0005887; C:Mitochondrion; TAS.
DR	GO; GO:0005739; C:Mitochondrion; TAS.
DR	GO; GO:0015207; F:Adenine transporter activity; TAS.
DR	GO; GO:0006091; P:energy pathways; TAS.
DR	GO; GO:0000002; P:mitochondrial genome maintenance; TAS.
DR	GO; GO:0006832; P:small molecule transport; TAS.
DR	InterPro; IPR002067; Mit_carrier.
DR	InterPro; IPR002030; Mit_uncoupling.
DR	InterPro; IPR001993; Mitoch_carrier.
DR	Pfam; PF00153; mito_carr; 3.
DR	PRINTS; PR00926; MITOCARRIER.
DR	PRINTS; PR00784; MITOCOUPLING.
DR	PROSITE; PS00215; MITOCH_CARRIER; 3.
KM	Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport; Multigene family; Disease mutation.
KW	TRANSMEM 12 29 1 (POTENTIAL).
FT	TRANSMEM 73 91 2 (POTENTIAL).
FT	TRANSMEM 117 134 3 (POTENTIAL).
FT	TRANSMEM 176 195 4 (POTENTIAL).
FT	TRANSMEM 214 231 5 (POTENTIAL).
FT	TRANSMEM 273 291 6 (POTENTIAL).
FT	REPEAT 1 110 1.
FT	REPEAT 111 208 2.
FT	REPEAT 209 298 3.
FT	REPEAT 114 114 A -> P (IN PEO).
FT	VARIANT 289 289 V -> M (IN PEO).
FT	CONFLICT 16 16 FTID=VAR_012112.
FT	CONFLICT 147 149 G -> A (IN REF. 3).
FT	CONFLICT 227 227 KGA -> RR (IN REF. 3).
FT	SEQUENCE 298 AA; 33064 MW; 59F0DPAEC4E7FBB CRC64;
QY	Query Match 91.3%; Score 1409; DB 1; Length 298;
DB	Best Local Similarity 88.3%; Pred. No. 2,1e-116;
DB	Matches 263; Conservative 19; Mismatches 16; Indels 0; Gaps 0;
DB	1 MTEQAIISPAKPLAGGIAAIAISKTAVADIERVKLLIQVHASKQIADKQYGVDCIVR 60
DB	1 MGDHAWSTLKFGLGVAANAASKTAVADIERVKLLIQVHASKQISAEKQYGIIDCVRR 60
DB	61 IPKQGVSTFMRGNANTYIRFPPOALNPAFADKQKQIFLGVDKQHTQFWRFAGNLSG 120
DB	61 IPKQGVSTFMRGNANTYIRFPPOALNPAFADKQKQIFLGVDKQHTQFWRFAGNLSG 120

Oy		121	GAAATATGTCFPPYLPDPARTRLAADAVGSQREBERGGDDCVKTKESDGRGLYGQSPVS	180
Oy		121	GAAATATGTCFPPYLPDPARTRLAADAVGSQREBERGGDDCVKTKESDGRGLYGQSPVS	180
Db		121	GAAATATGTCFPPYLPDPARTRLAADAVGSQREBERGGDDCVKTKESDGRGLYGQSPVS	180
Oy		181	VGGIITVRAAYFGVYDTAKGMLPDKXNTHIVSMWMIQTVTAAGVSVSYPFDVRRMM	240
Db		181	VGGIITVRAAYFGVYDTAKGMLPDKXNTHIVSMWMIQTVTAAGVSVSYPFDVRRMM	240
Oy		241	QSQRKKADIWYTGTGVDCWRKIIFRPEGKAFFPKAMSVVLAKMGAFVLVLYDEIKKYI	298
Db		241	QSQRKKADIWYTGTGVDCWRKIIFRPEGKAFFPKAMSVVLAKMGAFVLVLYDEIKKYI	298

  

```

RESULT 10
ADT_DROME STANDARD; PRT; 299 AA.
ID ADT_DROME
AC Q26365; P01614; Q26254; Q95S30; Q9VZ70;
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADP carrier protein (ADP/ATP translocase) (Adenine nucleotide
translocator) (ANT) (Stress sensitive B protein).
OS SESB OR A/A-T OR CG16944.
OC Drosophila melanogaster (Fruit fly).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Empidoidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RN RN
RP SEQUENCE FROM N.A.
RX RX MEDLINE=92389367; PubMed=1387687;
RA RA "A cDNA clone encoding the ADP/ATP translocase of Drosophila
RT RT melanogaster shows a high degree of similarity with the mammalian
RL RL ADP/ATP translocase."
RN RN J. Mol. Evol. 35:44-50(1992).
[2]
RN RN
RP SEQUENCE FROM N.A.
RX RX MEDLINE=94350065; PubMed=7520869;
RA RA Hutter P., Karch F.;
RT RT "Molecular analysis of a candidate gene for the reproductive
RL RL isolation between sibling species of Drosophila."
RN RN Experientia 50:749-762(1994).
[3]
RN RN
RP SEQUENCE FROM N.A.
RC RC STRAIN=Oregon-R;
RA RA Zhang Y.Q., Davis A.W., Roote J., Herrmann S., Ashburner M.;
RL RL Submitted (Jan-1997) to the EMBL/GenBank/DDBJ databases.
[4]
RN RN
RP SEQUENCE FROM N.A.
RC RC STRAIN=Berkley;
RX RX MEDLINE=20196006; PubMed=10731132;
RA RA Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Megnaatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Suton G.C., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.F., Baau A.B., Bakendale U., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhattacharya D., Bolintinas S.,
RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A.S., Chandra I.,
RA Cherry J.M., Chuang A., Dahlke C., Davenport L.B., Davies P.,
RA De Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dubnin K.U., Evangelista C.C., Feriz C., Ferreria S., Fleischmann W.,
RA Foster C., Gioleris A.E., Gary N.S., Gelbart W.M., Glasner K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.E., Ketchum K.A.,

```

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laaso P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spreading A.C., Stapleton M., Strong R., Sun E.,  
 RA Svrtek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*."; Science 287:2185-2195 (2000).  
 RL  
 RN  
 RP  
 RC STRAIN=Berkelley; TISSUE=Larva, Ovary, and Pupa;  
 RX MEDLINE=2242606; PubMed=12537569;  
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,  
 RA George R.A., Guatrin H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,  
 RA Rubin G.M., Celisner S.E.;  
 RT "A *Drosophila* full-length cDNA resource."; Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.6(2002).  
 CC  
 CC -1- FUNCTION: Catalyzes the exchange of ADP and ATP across the  
 CC mitochondrial inner membrane.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane (By similarity).  
 CC -1- DOMAIN: Composed of three homologous domains.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; S43651; AAB23114.1; -;  
 CC EMBL; S71762; AAB31734.3; -;  
 CC EMBL; Y10618; CA971628.1; -;  
 CC EMBL; AE003484; AAF47957.1; -;  
 CC EMBL; AY060978; AAL48526.1; -;  
 CC EMBL; AY070894; AAL48526.1; -;  
 CC FLYBASE; FBgn0003360; seeb.  
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEBC.  
 DR GO; GO:0006839; P:mitochondrial transport; IMP.  
 DR InterPro; IPR002067; Mlt\_carrier.  
 DR InterPro; IPR001993; Mltch\_carrier.  
 DR Pfam; PF00153; mltc\_carrier; 2.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.  
 FT TRANSMEM 14 31 1 (POTENTIAL).  
 FT TRANSMEM 75 93 2 (POTENTIAL).  
 FT TRANSMEM 119 136 3 (POTENTIAL).  
 FT TRANSMEM 177 196 4 (POTENTIAL).  
 FT TRANSMEM 215 232 5 (POTENTIAL).  
 FT TRANSMEM 274 292 6 (POTENTIAL).  
 FT TRANSMEM 18 19 G -> QV (IN REF. 1 AND 2).  
 FT TRANSMEM 81 81 I -> Y (IN REF. 1).  
 FT TRANSMEM 201 201 MISSING (IN REF. 1 AND 2).  
 FT TRANSMEM 267 267 G -> A (IN REF. 2).  
 FT TRANSMEM 268 269 TG -> P (IN REF. 1 AND 2).  
 FT TRANSMEM 270 270 A -> S (IN REF. 1).  
 FT TRANSMEM 270 270 A -> C (IN REF. 2).  
 FT TRANSMEM 299 AA; 32909 MW; D51F3E2A70BD59E8 CRC64;  
 SQ SEQUENCE

Query Match 81.3%; Score 1254.5; DB 1; Length 299;  
 Best Local Similarity 80.6%; Pred. No. 7.5e-103;  
 Matches 237; Conservative 23; Mismatches 33; Indels 1; Gaps 1;  
 QY 5 AISPADKDLAAGIAAIAIKTAVAPIERVKLLQVHASKQIADKQYGYDCTIRIPE 64  
 DB 7 AVGFQKDAAGISAAVSKTAVAPIERVKLLQVHASKQIADKQYGYDCTIRIPE 66  
 QY 65 QGVSSFWGNLANVRYPTALNPAFDKKQVFLGVDVNDHTQWRFPAGLASSGAAG 124  
 DB 67 QGVSSFWGNLANVRYPTALNPAFDKKQVFLGVDVNDHTQWRFPAGLASSGAAG 126  
 QY 125 ATSLCFVYPLDFARTLADVKGSGTEREFGDCLVKTIKSDIRGLYGSFVSVOGI 184  
 DB 127 ATSLCFVYPLDFARTLADVKGSGTEREFGDCLVKTIKSDIRGLYGSFVSVOGI 185  
 QY 185 IYRAAYGVYDTAKMLPDPKNTIIVSMIAQTVAAGVSYPTVRRMMQSGR 244  
 DB 186 IYRAAYGVYDTAKMLPDPKNTIIVSMIAQTVAAGVSYPTVRRMMQSGR 245  
 QY 245 KGADIMYGTVDCKRKIRFDEGKAFKFGASNVLRMGCAFVLVYDELKVI 298  
 DB 246 KATEVINYNTLHCWATIAKQEGTGAFFKGAFFSNILRTGGAFLVLYDEIKKV 299  
 RESULT 11  
 ADT\_ANOGA  
 ID ADT\_ANOGA STANDARD; PRT; 301 AA.  
 AC Q27238;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE ADP, ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide  
 DE translocator) (ANT).  
 OS Anopheles gambiae (African malaria mosquito).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.  
 OX NCBI\_Taxid=7165;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=G3;  
 RX MEDLINE=94348635; PubMed=8069414;  
 RT Beard C.B., Crews-Oyen A.E., Kumar V.K., Collins F.H.;  
 RT "A cDNA encoding an ADP/ATP carrier from the mosquito *Anopheles*  
 RT *gambiae*."; Insect Mol. Biol. 3:35-40(1994).  
 RL  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; L11618; AAB04104.1; -;  
 CC EMBL; L11617; AAB04105.1; -;  
 CC InterPro; IPR002067; Mlt\_carrier.  
 CC InterPro; IPR001993; Mltch\_carrier.  
 CC Pfam; PF00153; mltc\_carrier; 3.  
 CC PRINTS; PR00926; MITOCARRIER.  
 CC PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.  
 FT TRANSMEM 14 31 1 (POTENTIAL).  
 FT TRANSMEM 75 93 2 (POTENTIAL).  
 FT TRANSMEM 119 136 3 (POTENTIAL).  
 FT TRANSMEM

Query Match 78.0%; Score 1204; DB 1; Length 301;  
Best Local Similarity 77.7%; Pred. No. 2,1e-98;  
Matches 233; Conservative 23; Mismatches 42; Indels 2; Gaps 1;

Query 1 MTEGA--ISFAKDLAGGIAAISKTAVERKLLQVQHASKQIAADKQVGIYDCI 58  
Db 1 MTKADADYGAPOKFLAGISAAVSKTAVAPLBRKLLQVQASAKQIAVDKQVGIYDCP 60

Query 59 VRIPEKOGVIFWFGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLA 118  
Db 61 VRIPEKOGVIFWFGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLA 120

Query 119 SGGAAGATSLCFVYPLDPAFTRILADVGKSGTEREFGDGLVKTSGDGRGLYOGFS 178  
Db 121 SGGAAGATSLCFVYPLDPAFTRILADVGKSGTEREFGDGLVKTSGDGRGLYOGFS 180

Query 179 VSVGGIITVRAAYGVYDTAKGMLPDPKNTHTVSNMIAQVTVAAGVSYPTVRRRM 238  
Db 181 VSVGGIITVRAAYGVYDTAKGMLPDPKNTHTVSNMIAQVTVAAGVSYPTVRRRM 240

Query 239 MMOSGRKADIMYGTVDCKRKIFRDEGKAFKFGKANSNVLRGGAFAVLVYDELKKVI 298  
Db 241 MMOSGRKADIMYGTVDCKRKIFRDEGKAFKFGKANSNVLRGGAFAVLVYDELKKVI 300

RESULT 12  
ADT\_CHLKE STANDARD; PRT; 339 AA.

AC P1692;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).  
OS Chlorella kessleri;  
OC Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales; OC Chlorellaceae; Chlorella.  
ON NCBI\_TaxID=3074;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92084708; PubMed=1748677;  
RA Hilgath C., Sauer N., Tanner W.;  
RT "Glucose increases the expression of the ATP/ADP translocator and the glyceraldehyde-3-phosphate dehydrogenase genes in Chlorella.";  
RL J. Biol. Chem. 266:24044-24047(1991).  
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.  
CC -1- SUBUNIT: Homodimer (By similarity).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.  
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).

CC EMBL; M76669; AAA33027.1; -  
CC PIR; A41677; A41677;  
DR InterPro: IPR002067; Mit\_carrier  
DR InterPro: IPR001993; Mitoch\_carrier  
DR Pfam; PF00153; mito\_carr; 3.  
DR PRINTS; PR00926; MITOCHARRIER.  
DR PROSITE; PS00215; MITOCH\_CARRIER; 3.

Query Match 63.4%; Score 978; DB 1; Length 339;  
Best Local Similarity 66.9%; Pred. No. 1.6e-78;  
Matches 198; Conservative 26; Mismatches 64; Indels 8; Gaps 5;

Query 6 ISFAKDLAGGIAAISKTAVERKLLQVQHASKQIAADK--QYKGIYDCIYRIPK 63  
Db 39 MAFVKDLAGGTAAGISAKTAVERKLLQVQDSNPMKSGQVPRYTIVNCFYVSS 98

Query 64 EGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLAGAA 123  
Db 99 EGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLAGAA 157

Query 124 GATSLCFVYPLDPAFTRILADVGKSGTEREFGDGLVKTSGDGRGLYOGFSVVOG 183  
Db 158 GATSLCFVYPLDPAFTRILADVG--SGKSREFTGLVDCLSKVRRGGMALYOGFSVVOG 216

Query 184 IIVRAAYGVYDTAKGMLPDPKNTHTVSNMIAQVTVAAGVSYPTVRRRMQOS 242  
Db 217 IIVRAAYGVYDTAKGMLPDPKNTHTVSNMIAQVTVAAGVSYPTVRRRMQOS 276

Query 243 GRRGADIMYGTVDCKRKIFRDEGKAFKFGKANSNVLRGGAFAVLVYDELKKVI 298  
Db 277 ---GGRGADIMYGTVDCKRKIFRDEGKAFKFGKANSNVLRGGAFAVLVYDELKKVI 329

RESULT 13  
ADT\_YEAST STANDARD; PRT; 307 AA.

ID ADT3\_YEAST  
AC P18238;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE ADP/ATP carrier protein 3 (ADP/ATP translocase 3) (Adenine nucleotide translocator 3) (ANT 3).  
GN AAC3 OR YBR085W OR YBR0753.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
ON NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90324269; PubMed=2165073;  
RA Kolacov J., Kolacova N., Nelson N.;  
RT "A third ADP/ATP translocator gene in yeast.";  
RL J. Biol. Chem. 265:12711-12716(1990).  
CC [2]  
CC SEQUENCE FROM N.A.  
CC STRAIN=S288C;  
RA Andre B., Cziepluch C., Hein C., Jauniaux J.C., Urrestarazu A.,  
RA Visseers S.;  
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 38-307 FROM N.A.  
RC STRAIN=S288C;  
RA Feldmann H., Mannhaupt G., Schwarzlose C., Vetter I.;  
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.  
CC -1- SUBUNIT: Homodimer.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.  
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; M34076; AAA97485.1; -  
 DR EMBL; Z35954; CAA85031.1; -  
 DR PIR; A36582; A36582.  
 DR SCD; S0000289; AAC3.  
 DR GO; GO:0005471; F:ATP/ADP antiporter activity; IMP.  
 DR GO; GO:0006854; P:ATP/ADP exchange; IMP.  
 DR InterPro; IPR002067; Mlt\_carrier.  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR Pfam; PF00153; mito\_carr; 3.  
 DR PRINTS; PR00926; MITOCH\_CARRIER.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 2.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KW Multigene family.  
 FT TRANSMEM 16 33 1 (POTENTIAL).  
 FT TRANSMEM 78 96 2 (POTENTIAL).  
 FT TRANSMEM 120 137 3 (POTENTIAL).  
 FT TRANSMEM 181 200 4 (POTENTIAL).  
 FT TRANSMEM 220 237 5 (POTENTIAL).  
 FT TRANSMEM 276 294 6 (POTENTIAL).  
 FT TRANSMEM 307 AA; 33313 MW; D0C1329FEC1BADC8 CRC64;  
 SQ SEQUENCE 307 AA; 33313 MW; D0C1329FEC1BADC8 CRC64;

Query Match 50.5%; Score 778.5; DB 1; Length 307;  
 Best Local Similarity 53.7%; Pred. No. 4.5e-61;  
 Matches 161; Conservative 45; Mismatches 85; Indels 9; Gaps 5;

QY 3 EQATSPADFLAGTAAISTAVAPIERVKLLQVQ-HASKQIADKQYKGIYDCTIRI 61  
 Db 7 QOETNFAINFLMGVSAIAIATAPIERVKILLIONDEMIKQGLDCKYGIYDCFRRT 66  
 QY 62 PKEOGVLSFMRGNLANVRYEPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLASGG 121  
 Db 67 AKQEGSLISFMGNANVRIEPTQALNFAFKDKITMT--GFKKEGSGKMFAGNLASGG 124  
 QY 122 AAGATSLCFVYPLDFARTRLADV--GKSGTEREFGIGDCLVKITKSDGIRGLYQGFVS 179  
 Db 125 AAGALSLFVYSLDFARTRLADAKSSKKGARQENGTLDYVKTLKSDGIAGLYRGFMP 184  
 QY 180 SVQGIITIRAAVFGVYDTAKGM-LPDPKNTIHVSMNIAQVTVTAAGVVSYPPTVRRM 238  
 Db 185 SVGIIVYRGVYFGVYDLPKLVLAGSLDGSFLASFLGLGWVVTTCASVYPLDVRRRM 244  
 QY 239 MMOSGRKGAADIMYGTVDCKWKIFRDEGKAFFKGSANVLRGNGAFVLVLYDELKVI 298  
 Db 245 MMTSGQA--VKYNGAIDCLKKIVASBGVSLFKCGGANILRSVAGAVISMVDOLOMTL 301

RESULT 14  
 ADT\_CHLRE STANDARD; PRT; 308 AA.  
 ID ADT\_CHLRE  
 AC P27080.  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE ADP carrier protein (ADP/ATP translocase) (Adenine nucleotide  
 DE translocator) (ANT).  
 GN Ant.  
 OS Chlamydomonas reinhardtii.  
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;  
 OC Chlamydomonadaceae; Chlamydomonas.  
 OX NCBI\_TaxID=3055;  
 OX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FUD44-R2;  
 RX MEDLINE=93204887; PubMed=8455552;  
 RA Sharpe J.A., Day A.;

RT "Structure, evolution and expression of the mitochondrial ADP/ATP  
 RT translocator gene from Chlamydomonas reinhardtii.";  
 RL Mol. Gen. Genet. 237:134-144(1993).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
 CC -1- This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; X65194; CAA46311.1; -  
 DR PIR; S30259; S30259.  
 DR InterPro; IPR002067; Mlt\_carrier.  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR Pfam; PF00153; mito\_carr; 3.  
 DR PRINTS; PR00926; MITOCH\_CARRIER.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 2.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.  
 FT TRANSMEM 12 29 1 (POTENTIAL).  
 FT TRANSMEM 74 92 2 (POTENTIAL).  
 FT TRANSMEM 116 133 3 (POTENTIAL).  
 FT TRANSMEM 178 197 4 (POTENTIAL).  
 FT TRANSMEM 217 234 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT TRANSMEM 308 AA; 33528 MW; D477CF0E72B7A53F CRC64;  
 SQ SEQUENCE 308 AA; 33528 MW; D477CF0E72B7A53F CRC64;

Query Match 50.0%; Score 772; DB 1; Length 308;  
 Best Local Similarity 51.8%; Pred. No. 1.7e-60;  
 Matches 157; Conservative 55; Mismatches 81; Indels 10; Gaps 5;

QY 1 MTEQATSPADFLAGTAAISTAVAPIERVKLLQVQ-HASKQIADKQYKGIYDCTIRI 59  
 Db 1 MAKEEKFMVDFLAGGSAVASKTAAPIERVKILLIONDEMIKQGLASPYKIGICFV 60  
 QY 60 RPEQGVLSFMRGNLANVRYEPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLAS 119  
 Db 61 RTVEBEGSLMRGNLANVRYEPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLAS 118  
 QY 120 GGAAGATSLCFVYPLDFARTRLAAD--VGKSGTEREFGIGDCLVKITKSDGIRGLYQ 176  
 Db 119 GGAAGATSLSVYSLDFARTRLADAKSAGKGGADROPNGLVYRRTIASDGIAGLYRG 178  
 QY 177 FSVSVGIIITIRAAVFGVYDTAKG-MLPDPKNTIHVSMNIAQVTVTAAGVVSYPPTV 235  
 Db 179 FNISCVGIIVYRGVYFGVYDLPKLVLAGVPLANNFLAFLGMDGITGAGLASPIDTIR 238  
 QY 236 RRMNOSGRKGAADIMYGTVDCKWKIFRDEGKAFFKGSANVLRGNGAFVLVLYDELK 295  
 Db 239 RRMNMTS--GSAAVKNSSPHCFQELVNEGMSLFRGAGANITIRAAVAGAVLAGVDOLO 295  
 QY 296 KVI 298  
 Db 296 VIL 298

RESULT 15  
 ADT\_SCHPO STANDARD; PRT; 322 AA.  
 ID ADT\_SCHPO  
 AC O09188;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE ADP carrier protein (ADP/ATP translocase) (Adenine nucleotide  
 DE translocator) (ANT).  
 GN translocator (ANT).



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 18, 2003, 17:07:54 ; Search time 20 Seconds

(without alignments)  
1432.913 Million cell updates/sec

Title: US-09-185-904A-33

Perfect score: 1543  
Sequence: 1 MTEQALISFAKDFLAGIAAA.....LRGMGAFLVLYDELKKVI 298

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	298	1 S03894	ADP,ATP carrier pr
2	1512	98.0	298	2 B43646	ADP,ATP carrier pr
3	1454	94.2	298	1 A29132	ADP,ATP carrier pr
4	1424	92.3	298	2 I60173	adenine nucleotide
5	1422	92.2	298	1 XMBO	ADP,ATP carrier pr
6	1418	91.9	298	2 S37210	ADP,ATP carrier pr
7	1409	91.3	298	1 A44778	ADP,ATP carrier pr
8	1405	91.1	298	2 S31814	ADP,ATP carrier pr
9	1184	76.7	301	1 S31935	ADP,ATP carrier pr
10	1041	67.5	313	2 T3207	ADP,ATP carrier pr
11	1039	67.3	313	1 T25850	hypothetical prote
12	1038	67.3	300	2 T25371	hypothetical prote
13	993.5	64.4	300	2 T15205	hypothetical prote
14	978	63.4	339	2 A41677	ADP,ATP carrier pr
15	943	61.1	301	2 S51132	ADP,ATP carrier pr
16	778.5	50.5	307	2 A36582	ADP,ATP carrier pr
17	772	50.0	308	1 S30259	ADP,ATP carrier pr
18	769	49.8	322	2 T40526	ADP,ATP translocas
19	768	49.8	386	2 T09709	ADP,ATP carrier pr
20	766	49.6	313	1 XMNC	ADP,ATP carrier pr
21	764	49.5	326	2 T25728	hypothetical prote
22	762.5	49.4	305	2 S68154	ADP,ATP carrier pr
23	760.5	49.3	318	1 A31978	ADP,ATP carrier pr
24	756.5	49.0	306	2 T30012	hypothetical prote
25	750	48.6	387	2 S14876	ADP,ATP carrier pr
26	748	48.5	386	2 S21974	ADP,ATP carrier pr
27	747	48.4	306	2 T42011	ADP,ATP carrier pr
28	747	48.4	386	2 S17917	ADP,ATP carrier pr
29	744	48.2	387	2 S16568	ADP,ATP carrier pr

30	743	48.2	379	2 T04608	ADP,ATP carrier pr
31	742.5	48.1	385	1 S29852	ADP,ATP carrier pr
32	742	48.1	382	2 S33630	ADP,ATP carrier pr
33	739.5	47.9	386	2 S14874	ADP,ATP carrier pr
34	737.5	47.8	309	2 A24849	ADP,ATP carrier pr
35	734.5	47.6	379	2 S21313	ADP,ATP carrier pr
36	681.5	44.2	298	2 T24029	hypothetical prote
37	520.5	33.7	327	2 T51577	ADP/ATP translocas
38	383	24.8	325	2 T04273	hypothetical prote
39	381	24.7	352	2 T01729	mitochondrial solu
40	372	24.1	358	2 T45934	hypothetical prote
41	370.5	24.0	415	2 T48171	hypothetical prote
42	369.5	23.9	381	2 T51158	hypothetical prote
43	368	23.8	475	2 T50686	peroxisomal Ca-dep
44	363	23.5	448	2 D84798	probable mitochond
45	344.5	22.3	332	2 T47703	Ca-dependent solut

## ALIGNMENTS

## RESULT 1

S03894  
ADP,ATP carrier protein T3 - human  
N/Alternate names: ADP,ATP carrier protein T2 (misidentification); mitochondrial ADP,ATP  
C/Species: Homo sapiens (man)  
C/Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 17-Mar-2000  
C/Accession: S03894; B28116  
R/Cozens, A.L.; Runswick, M.J.; Walker, J.E.  
J. Mol. Biol. 206, 261-280, 1989  
A/Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr  
A/Reference number: S03893; MUID:89236396; PMID:2541251  
A/Accession: S03854  
A/Status: not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-298 <CO2>  
R/Houldsworth, J.; Attardi, G.  
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988  
A/Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a  
A/Reference number: A94197; MUID:86124845; PMID:2829183  
A/Accession: B28116  
A/Molecule type: mRNA  
A/Residues: 36-104, 'R', 106, 'A', 109-298 <HO2>  
A/Reference number: GB:J03592; NID:g339722; PIDN:AAA36750.1; PID:g339723  
A/Experimental source: liver  
C/Genetics:  
A/Gene: GDB:ANT3; ANT3Y  
A/Cross-references: GDB:125184; OMIM:300151; OMIM:403000  
A/Map position: Xp22.32-Xp22.33; Yp11.3-Yp11.3  
A/Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and GDB:  
C/Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology  
C/Keywords: duplication; homodimer; mitochondrion; transmembrane protein  
F:2-298/Product: ADP,ATP carrier protein #status predicted <MAT>  
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>  
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>  
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 100.0%; Score 1543; DB 1; Length 298;

Best local similarity 100.0%; Pred. No. 6e-129;

Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MTEQALISFAKDFLAGIAAISKTAVPRIERVKLLLOVHASQIADADKQYGVDCIVR	60
Db	1	MTEQALISFAKDFLAGIAAISKTAVPRIERVKLLLOVHASQIADADKQYGVDCIVR	60
Qy	61	IPKEQGLSFWRGUINAVIRYPTQALNFAFKDKYKQIFLGGVDKHTQFRYFAGNLASG	120
Db	61	IPKEQGLSFWRGUINAVIRYPTQALNFAFKDKYKQIFLGGVDKHTQFRYFAGNLASG	120
Qy	121	GAAGATSLCFVYPIIDFARTRILADVGVKSGTEREERFGIGDCLVITKYSQDGIKGLYOGFSVS	180
Db	121	GAAGATSLCFVYPIIDFARTRILADVGVKSGTEREERFGIGDCLVITKYSQDGIKGLYOGFSVS	180



QY 181 VGGIIIRAAVFGVYDTAKGMLPDPKXTHIVSWMIQVTAAGVSYFEDTVRRMM 240  
 |||  
 DB 181 VGGIIIRAAVFGVYDTAKGMLPDPKXTHIVSWMIQVTAAGVSYFEDTVRRMM 240  
 |||  
 QY 241 QSGRKGADIMYTGTVDCMRKI FRDEGGKAFKFGKAMSVNLGKGAFVLVYDELKVI 298  
 |||  
 DB 241 QSGRKGADIMYTGTVDCMRKI FRDEGGKAFKFGKAMSVNLGKGAFVLVYDELKVI 298  
 |||

## RESULT 2

B43646  
 ADP/ATP carrier protein T2 - bovine  
 C/Species: Bos primigenius taurus (cattle)  
 C/Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 20-Aug-1999  
 C/Accession: B43646  
 R/Powell, S.U.; Medd, S.M.; Runswick, M.J.; Walker, J.E.  
 Biochemistry 28, 866-873, 1989  
 A/Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in  
 F/110-202/Domain: ADP/ATP carrier protein repeat homology <ACP3>  
 F/207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>  
 A/Accession: B43646  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-298 <POM>  
 A/Cross-references: GB:M24103; NID:9529416; PIDN:AAA30769.1; PID:9529417  
 C/Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology  
 C/Keywords: duplication; homodimer; mitochondrion; transmembrane protein  
 F/5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>  
 F/110-202/Domain: ADP/ATP carrier protein repeat homology <ACP3>  
 F/207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 98.0%; Score 1512; DB 2; Length 298;  
 Best Local Similarity 97.7%; Pred. No. 3,3e-126;  
 Matches 291; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTEQAISFADPLAGGIAAIAISTAVAPIERVKLLQVQHASQIADKQYKGIIDCVIR 60  
 |||  
 DB 1 MTEQAISFADPLAGGIAAIAISTAVAPIERVKLLQVQHASQIADKQYKGIIDCVIR 60  
 |||  
 QY 61 IPEQGVLSFWRGNLAVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLSG 120  
 |||  
 DB 61 IPEQGVLSFWRGNLAVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLSG 120  
 |||  
 QY 121 GAAGATSLCFVYPLDFARTRLAADVKGSTEREFRGLGDCLVKITSKGIRGLYQGFVS 180  
 |||  
 DB 121 GAAGATSLCFVYPLDFARTRLAADVKGSTEREFRGLGDCLVKITSKGIRGLYQGFVS 180  
 |||  
 QY 181 VGGIIIRAAVFGVYDTAKGMLPDPKXTHIVSWMIQVTAAGVSYFEDTVRRMM 240  
 |||  
 DB 181 VGGIIIRAAVFGVYDTAKGMLPDPKXTHIVSWMIQVTAAGVSYFEDTVRRMM 240  
 |||  
 QY 241 QSGRKGADIMYTGTVDCMRKI FRDEGGKAFKFGKAMSVNLGKGAFVLVYDELKVI 298  
 |||  
 DB 241 QSGRKGADIMYTGTVDCMRKI FRDEGGKAFKFGKAMSVNLGKGAFVLVYDELKVI 298  
 |||

## RESULT 3

A29132  
 ADP/ATP carrier protein T2 - human  
 N/Alternate names: mitochondrial ADP/ATP translocase 2  
 C/Species: Homo sapiens (man)  
 C/Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 17-Mar-2000  
 C/Accession: A29132; C28116  
 R/Battini, R.; Ferrarini, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.  
 J. Biol. Chem. 267, 4355-4359, 1987  
 A/Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulat  
 A/Reference number: A29132; MUID:8716056; PMID:3031073  
 A/Accession: A29132  
 A/Molecule type: mRNA  
 A/Residues: 1-298 <BAT>  
 A/Cross-references: GB:002663; NID:9179246; PIDN:AAA35579.1; PID:9179247  
 R/Houldsworth, J.; Attardi, G.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988  
 A/Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a

A/Reference number: A94197; MUID:88124845; PMID:2829183  
 A/Accession: C28116  
 A/Molecule type: mRNA  
 A/Residues: 47-65, 'G', 67-110, 'L', 112-161, 'G', 163-298 <HOU>  
 A/Cross-references: GB:003591; NID:9339720; PIDN:AAA56749.1; PID:9339721  
 A/Experimental source: clone PHAT3  
 A/Genetics:  
 A/Gene: GDB:ANT2; T3; 2P1  
 A/Cross-references: GDB:125190; OMIM:300150  
 A/Map position: Xq13-Xq26  
 A/Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and GDB:J

C/Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology  
 C/Keywords: duplication; homodimer; mitochondrion; transmembrane protein  
 F/5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>  
 F/110-202/Domain: ADP/ATP carrier protein repeat homology <ACP3>  
 F/207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 94.2%; Score 1454; DB 1; Length 298;  
 Best Local Similarity 92.6%; Pred. No. 4.5e-121;  
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQAISFADPLAGGIAAIAISTAVAPIERVKLLQVQHASQIADKQYKGIIDCVIR 60  
 |||  
 DB 1 MTEQAISFADPLAGGIAAIAISTAVAPIERVKLLQVQHASQIADKQYKGIIDCVIR 60  
 |||  
 QY 61 IPEQGVLSFWRGNLAVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLSG 120  
 |||  
 DB 61 IPEQGVLSFWRGNLAVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLSG 120  
 |||  
 QY 121 GAAGATSLCFVYPLDFARTRLAADVKGSTEREFRGLGDCLVKITSKGIRGLYQGFVS 180  
 |||  
 DB 121 GAAGATSLCFVYPLDFARTRLAADVKGSTEREFRGLGDCLVKITSKGIRGLYQGFVS 180  
 |||  
 QY 181 VGGIIIRAAVFGVYDTAKGMLPDPKXTHIVSWMIQVTAAGVSYFEDTVRRMM 240  
 |||  
 DB 181 VGGIIIRAAVFGVYDTAKGMLPDPKXTHIVSWMIQVTAAGVSYFEDTVRRMM 240  
 |||  
 QY 241 QSGRKGADIMYTGTVDCMRKI FRDEGGKAFKFGKAMSVNLGKGAFVLVYDELKVI 296  
 |||  
 DB 241 QSGRKGADIMYTGTVDCMRKI FRDEGGKAFKFGKAMSVNLGKGAFVLVYDELKVI 296  
 |||

## RESULT 4

160173  
 adenine nucleotide translocator - rat  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 20-Aug-1999  
 C/Accession: 160173  
 R/Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.  
 Biochim. Biophys. Acta 1152, 192-196, 1993  
 A/Title: Isolation and characterization of cDNA clones and a genomic clone encoding rat n  
 A/Reference number: 160173; MUID:94002161; PMID:8393300  
 A/Accession: 160173  
 A/Status: preliminary; translated from GB/EMBL/DDJ  
 A/Molecule type: DNA  
 A/Residues: 1-298 <RES>  
 A/Cross-references: EMBL:X61667; NID:9400426; PIDN:CAA43842.1; PID:9400427  
 C/Genetics:  
 A/Gene: anti1  
 A/Intons: 37/3; 200/1; 247/1  
 C/Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology  
 C/Keywords: duplication; transmembrane protein  
 F/5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>  
 F/110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>  
 F/207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 92.3%; Score 1424; DB 2; Length 298;  
 Best Local Similarity 89.6%; Pred. No. 2e-118;  
 Matches 267; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQAISFADPLAGGIAAIAISTAVAPIERVKLLQVQHASQIADKQYKGIIDCVIR 60  
 |||  
 DB 1 MTEQAISFADPLAGGIAAIAISTAVAPIERVKLLQVQHASQIADKQYKGIIDCVIR 60  
 |||



QY 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120  
Db 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120  
QY 121 GAAGATSLCFYVPLDPFARTRLAADVGSCTERBERFGDCLVTKTSQDITRGLYQGFVS 180  
Db 121 GAAGATSLCFYVPLDPFARTRLAADVGSCTERBERFGDCLVTKTSQDITRGLYQGFVS 180  
QY 181 VGGIITRYAAFGVYDPAKGMPLDPKNTHTIIVSMIAQVTAVAGVSYPPDTRRRMM 240  
Db 181 VGGIITRYAAFGVYDPAKGMPLDPKNTHTIIVSMIAQVTAVAGVSYPPDTRRRMM 240  
QY 241 QSGRGADIMYTGTVDCWRKIFRDEGKAFPKGAMSNVLRGMGAFVLVLYDELKKVI 298  
Db 241 QSGRGADIMYTGTVDCWRKIFRDEGKAFPKGAMSNVLRGMGAFVLVLYDELKKVI 298

RESULT 5

XMB0  
ADP, ATP carrier protein T1 - bovine  
N:Alternate names: ADP/ATP translocase T1  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 14-Nov-1983 #sequence revision 22-Jul-1994 #text\_change 22-Jun-1999  
C:Accession: A43646; A24822; A03181; A61343; S69369  
R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.  
Biochemistry 28, 866-873, 1989  
A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in  
A:Reference number: A43646; MUID:89229093; PMID:2540808  
A:Accession: A43646  
A:Molecule type: mRNA  
A:Residues: 1-298 <POM>  
A:Cross-references: GB:M24102; NID:9529414; PIDN:AAA30768.1; PID:9529415  
R:Rasmussen, U.B.; Wohlb, H.  
Biochem. Biophys. Res. Commun. 138, 850-857, 1986  
A:Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual  
A:Reference number: A24822; MUID:86295775; PMID:3017341  
A:Accession: A24822  
A:Molecule type: mRNA  
A:Residues: 208-298 <RAS>  
A:Cross-references: GB:M13783; NID:9162630; PIDN:AAA30363.1; PID:9162631  
R:Aquila, H.; Mistr, D.; Eulitz, M.; Klingenberg, M.  
Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982  
A:Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondria  
A:Reference number: A03181; MUID:82188267; PMID:7076130  
A:Accession: A03181  
A:Molecule type: Protein  
A:Residues: 2-51, 'X', '53-70, 'X', '72-109, 'X', '111-298 <AGU>  
A:Note: residue 52 may be methyllysine  
R:Babel, W.; Machter, E.; Aquila, H.; Klingenberg, M.  
Biochim. Biophys. Acta 670, 176-180, 1981  
A:Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitoch  
A:Reference number: A61343; MUID:82046808; PMID:6271240  
A:Accession: A61343  
A:Molecule type: Protein  
A:Residues: 205-298 <BAB>  
R:Oertmeier, W.; Masson, K.; Kalina, S.  
Eur. J. Biochem. 227, 730-733, 1995  
A:Title: [(3)H]-7-azido-4-isopropylacridone labels Cys159 of the bovine mitochondrial ADP  
A:Reference number: S69369; MUID:95172058; PMID:7867632  
A:Accession: S69369  
A:Molecule type: Protein  
A:Residues: 49-63, 154-168 <OET>  
C:Comment: This protein is synthesized in the cytosol and transported into the mitochond  
C:Complex: homodimer  
C:Function:  
A:Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP genera  
A:Note: located in the inner mitochondrial membrane  
C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology  
C:Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitoch  
F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>  
F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>  
F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental  
F:52/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 92.2%; Score 1422; DB 1; Length 298;  
Best Local Similarity 89.3%; Pred. No. 3, 1e-118;  
Matches 266; Conservative 19; Mismatches 13; Indels 0; Gaps 0;  
QY 1 MTEQAISPAKDFLAGGIAAISKTAVAPIEVEVKLLQVQHASKOIADKOYKGIIDCVR 60  
Db 1 MSDQALSLKDFLAGGVAIAISKTAVAPIEVEVKLLQVQHASKOIADKOYKGIIDCVR 60  
QY 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120  
Db 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120  
QY 121 GAAGATSLCFYVPLDPFARTRLAADVGSCTERBERFGDCLVTKTSQDITRGLYQGFVS 180  
Db 121 GAAGATSLCFYVPLDPFARTRLAADVGSCTERBERFGDCLVTKTSQDITRGLYQGFVS 180  
QY 181 VGGIITRYAAFGVYDPAKGMPLDPKNTHTIIVSMIAQVTAVAGVSYPPDTRRRMM 240  
Db 181 VGGIITRYAAFGVYDPAKGMPLDPKNTHTIIVSMIAQVTAVAGVSYPPDTRRRMM 240  
QY 241 QSGRGADIMYTGTVDCWRKIFRDEGKAFPKGAMSNVLRGMGAFVLVLYDELKKVI 298  
Db 241 QSGRGADIMYTGTVDCWRKIFRDEGKAFPKGAMSNVLRGMGAFVLVLYDELKKVI 298

RESULT 6

ADP, ATP carrier protein T1 - mouse  
N:Alternate names: adenine nucleotide carrier  
C:Species: Mus musculus (house mouse)  
C>Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text\_change 20-Aug-1999  
C:Accession: S37210  
R:Laplace, C.; Coetzel, P.  
Submitted to the EMBL Data Library, September 1993  
A:Reference number: S37210  
A:Accession: S37210  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-298 <LAP>  
A:Cross-references: EMBL:X74510; NID:9402627; PIDN:CAA52616.1; PID:9402628  
C:Genetics:  
A:Gene: ANCI  
C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology  
C:Keywords: duplication; transmembrane protein  
F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>  
F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>  
F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>  
Query Match 91.9%; Score 1418; DB 2; Length 298;  
Best Local Similarity 88.9%; Pred. No. 6, 9e-118;  
Matches 265; Conservative 19; Mismatches 14; Indels 0; Gaps 0;  
QY 1 MTEQAISPAKDFLAGGIAAISKTAVAPIEVEVKLLQVQHASKOIADKOYKGIIDCVR 60  
Db 1 MGDQALSLKDFLAGGIAAISKTAVAPIEVEVKLLQVQHASKOIADKOYKGIIDCVR 60  
QY 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120  
Db 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120  
QY 121 GAAGATSLCFYVPLDPFARTRLAADVGSCTERBERFGDCLVTKTSQDITRGLYQGFVS 180  
Db 121 GAAGATSLCFYVPLDPFARTRLAADVGSCTERBERFGDCLVTKTSQDITRGLYQGFVS 180  
QY 181 VGGIITRYAAFGVYDPAKGMPLDPKNTHTIIVSMIAQVTAVAGVSYPPDTRRRMM 240  
Db 181 VGGIITRYAAFGVYDPAKGMPLDPKNTHTIIVSMIAQVTAVAGVSYPPDTRRRMM 240  
QY 241 QSGRGADIMYTGTVDCWRKIFRDEGKAFPKGAMSNVLRGMGAFVLVLYDELKKVI 298  
Db 241 QSGRGADIMYTGTVDCWRKIFRDEGKAFPKGAMSNVLRGMGAFVLVLYDELKKVI 298

Db 241 OSGRKADIMYTGTLDCWRKIADKDEGANAFKGMASVLRGMGAFVLVLYDEIKKYV 298

## RESULT 7

ADP, ATP carrier protein T1 - human  
 N:Alternate names: mitochondrial ADP, ATP translocase 1  
 C/Species: Homo sapiens (man)  
 C/Date: 17-Mar-2000 #sequence revision 17-Mar-2000 #text\_change 17-Mar-2000  
 C/Accession: A44778; S03893; A39891; A28116  
 R/L1, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, M.  
 J. Biol. Chem. 264, 13998-14004, 1989  
 A>Title: A human muscle adenine nucleotide translocator gene has four exons, is located  
 A/Reference number: A44778; MUID:89340499; PMID:2547778  
 A/Accession: A44778  
 A>Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-298 <LTA>  
 A/Cross-references: GB:U04982; NID:G178658; PIDN:AAA51736.1; PID:G178659  
 R/Cozens, A.L.; Runswick, M.J.; Walker, J.E.  
 J. Mol. Biol. 206, 261-280, 1989  
 A>Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr  
 A/Reference number: S03893; MUID:89236396; PMID:2541251  
 A/Accession: S03893  
 A>Status: not compared with conceptual translation  
 A/Molecule type: DNA  
 A/Residues: 1-298 <COZ>  
 R/Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987  
 A>Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader  
 A/Reference number: A39891; MUID:88041149; PMID:2823266  
 A/Accession: A39891  
 A>Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-15, 'A', 17-146, 'RR', 149, 151-226, 'L', 228-298 <NEC>  
 A/Cross-references: GB:U02966; NID:G339919; PIDN:AAA61223.1; PID:G339920  
 A/Experimental source: clone pHMANT  
 R/Houldsworth, J.; Attardi, G.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988  
 A>Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a  
 A/Reference number: A94197; MUID:88124845; PMID:2829183  
 A/Accession: A28116  
 A/Molecule type: mRNA  
 A/Residues: 1-37 <HOU>  
 A/Cross-references: GB:J03593; NID:G339724; PIDN:AAA36751.1; PID:G339725  
 A/Experimental source: liver  
 C/Genetics:  
 A/Gene: GDB:ANT1; T1  
 A/Cross-references: GDB:119680; OMIM:103220  
 A/Map position: 4Q35-4Q35  
 C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology  
 C/Keywords: duplication; homodimer; mitochondrion; transmembrane protein  
 F;2-298/Product: ADP, ATP carrier protein #status predicted <MAT>  
 F;5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>  
 F;110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>  
 F;207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 91.3%; Score 1409; DB 1; Length 298;  
 Best Local Similarity 88.3%; Pred. No. 4.3e-117;  
 Matches 263; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTEQATSPADFLAGIAAIAISKTAVAPIERVKLLQVQHASKOIADKQYKGIIVDCTVR 60  
 Db 1 MGDHANSFLADFLAGVAAAVSKTAVAPIERVKLLQVQHASKOISERKQYKGIIVDCTVR 60  
 QY 61 IPKEQGLSFWRGKLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120  
 Db 61 IPKEQGLSFWRGKLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGIGDCLVKTSDGIRGLYOGFSVS 180  
 Db 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGIGDCLVKTSDGIRGLYOGFSVS 180  
 QY 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGIGDCLVKTSDGIRGLYOGFSVS 180  
 Db 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGIGDCLVKTSDGIRGLYOGFSVS 180

QY 181 VQGIITRYAAVFGVYDTAKGMLPDPKNTIHVSMWIAQVTAAGVVSYPEDTVRRMM 240  
 Db 181 VQGIITRYAAVFGVYDTAKGMLPDPKNTIHVSMWIAQVTAAGVVSYPEDTVRRMM 240  
 QY 241 OSGRKADIMYTGTVDCWRKIFPDEGKAFFKGMASVLRGMGAFVLVLYDEIKKYV 298  
 Db 241 OSGRKADIMYTGTVDCWRKIFPDEGKAFFKGMASVLRGMGAFVLVLYDEIKKYV 298

## RESULT 8

ADP, ATP carrier protein T2 - mouse  
 N:Alternate names: adenine nucleotide translocase  
 C/Species: Mus musculus (house mouse)  
 C/Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text\_change 09-Apr-1998  
 C/Accession: S31814  
 R/Colet, P.; Lapiere, C.  
 submitted to the EMBL Data Library, January 1993  
 A/Reference number: S31814  
 A/Accession: S31814  
 A>Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-298 <COS>  
 A/Cross-references: EMBL:X70847  
 C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology  
 C/Keywords: duplication; transmembrane protein  
 F;5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>  
 F;110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>  
 F;207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 91.1%; Score 1405; DB 2; Length 298;  
 Best Local Similarity 89.2%; Pred. No. 9.8e-117;  
 Matches 264; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTEQATSPADFLAGIAAIAISKTAVAPIERVKLLQVQHASKOIADKQYKGIIVDCTVR 60  
 Db 1 MTDAAVSFAKDFLAGVAAIAISKTAVAPIERVKLLQVQNTDRTIADKQYKGIIVDCTVR 60  
 QY 61 IPKEQGLSFWRGKLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120  
 Db 61 IPKEQGLSFWRGKLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGIGDCLVKTSDGIRGLYOGFSVS 180  
 Db 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFGIGDCLVKTSDGIRGLYOGFSVS 180  
 QY 181 VQGIITRYAAVFGVYDTAKGMLPDPKNTIHVSMWIAQVTAAGVVSYPEDTVRRMM 240  
 Db 181 VQGIITRYAAVFGVYDTAKGMLPDPKNTIHVSMWIAQVTAAGVVSYPEDTVRRMM 240  
 QY 241 OSGRKADIMYTGTVDCWRKIFPDEGKAFFKGMASVLRGMGAFVLVLYDEIKKYV 298  
 Db 241 OSGRKADIMYTGTVDCWRKIFPDEGKAFFKGMASVLRGMGAFVLVLYDEIKKYV 298

## RESULT 9

ADP, ATP carrier protein - African malaria mosquito  
 C/Species: Anopheles gambiae (African malaria mosquito)  
 C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C/Accession: S31935; S31936  
 R/Beard, C.B.; Crews-Owen, A.E.; Collins, F.H.  
 submitted to the EMBL Data Library, February 1993  
 A/Description: A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae.  
 A/Reference number: S31935  
 A/Accession: S31935  
 A/Molecule type: DNA  
 A/Status: preliminary  
 A/Residues: 1-301 <BEA>  
 A/Cross-references: EMBL:Z21814; EMBL:Z21815  
 C/Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology  
 C/Keywords: duplication; transmembrane protein  
 F;7-101/Domain: ADP, ATP carrier protein repeat homology <ACP1>

F:112-204/Domain: ADP,ATP carrier protein repeat homology <ACP2>  
F:209-300/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 76.7%; Score 1184; DB 1; Length 301;  
Best Local Similarity 77.0%; Pred. No. 3.6e-97;

Matches 231; Conservative 23; Mismatches 44; Indels 2; Gaps 1;

QY 1 MTEQA-1SFAKDLAAGIAAISTAVAPIERVKLLQVOHASKQIADKQYKIVICI 58  
DB 1 MTKKADPYGPAKDLAAGIAAISTAVAPIERVKLLQVOHASKQIADKQYKIVICI 60  
QY 59 VRIPEQGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFGVGDKHTQFMRYPAGNIA 118  
DB 61 VRIPEQGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFGVGDKHTQFMRYPAGNIA 120  
QY 119 SGGAAGATSLGCVNYPLDFAFRTLAADVKGSGTEREFGDCLVYKITSDDGIRGYOGFS 178  
DB 121 SGGAAGATSLGCVNYPLDFAFRTLAADVKGSGTEREFGDCLVYKITSDDGIRGYOGFS 180  
QY 179 VSVGGIITVRAAYFGVDTAKGMLPDPKNTHTVSWMTAQVTVAVAGVSYPTVRRRM 238  
DB 181 VSVGGIITVRAAYFGVDTAKGMLPDPKNTHTVSWMTAQVTVAVAGVSYPTVRRRM 240  
QY 239 MMOSGRKADIMYTGTVDCWRKIFRDEGSKAFKFGKAMSNTLRGMAFVLVLYDELKXYI 298  
DB 241 MMOSGRKADIMYTGTVDCWRKIFRDEGSKAFKFGKAMSNTLRGMAFVLVLYDELKXYI 300

# RESULT 10

T23207  
hypochemical protein K01H2.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 11-Jan-2000

C:Accession: T23207

R:McMurray, A.  
submitted to the EMBL Data Library, December 1995

A:Reference number: Z19707

A:Accession: T23207

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-313 <Wtl>

A:Cross-references: EMBL: Z68218; PIDN: CAA92472.1; GSPDB: GN00022; CESP: K01H2.2

A:Experimental source: clone K01H2

C:Genetics:

A:Gene: CESP:K01H2.2

A:Map position: 4

A:Introns: 4/1, 191/2

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 67.5%; Score 1041; DB 2; Length 313;  
Best Local Similarity 70.9%; Pred. No. 1.7e-84;

Matches 207; Conservative 29; Mismatches 52; Indels 4; Gaps 3;

QY 8 FAKDFLAGIAAISTAVAPIERVKLLQVOHASKQIADKQYKIVICI 67  
DB 25 FLIDLASGTAASAASKTAVAPIERVKLLQVOHASKQIADKQYKIVICI 84  
QY 68 LSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLAGGAAGTS 127  
DB 85 AALMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLAGGAAGTS 144  
QY 128 LCFVYPLDFAFRTLAADVKGSGTEREFGDCLVYKITSDDGIRGYOGFSVSGIITV 187  
DB 145 LCFVYPLDFAFRTLAADVKGSGTEREFGDCLVYKITSDDGIRGYOGFSVSGIITV 203  
QY 188 RAAVFGVDTAKGMLPDPKNTHTVSWMTAQVTVAVAGVSYPTVRRRMQSGRKG 246  
DB 204 RAAVFGVDTAKGMLPDPKNTHTVSWMTAQVTVAVAGVSYPTVRRRMQSGRKG 262  
QY 247 ADIMYTGTVDCWRKIFRDEGSKAFKFGKAMSNTLRGMAFVLVLYDELKXYI 298  
DB 263 -DVLYKNTLDCAVKITRDEGSKAFKFGKAMSNTLRGMAFVLVLYDELKXYI 313

# RESULT 11

T25850

hypochemical protein T01B11.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 11-Jan-2000

C:Accession: T25850

R:Geisel, C.; Stellyes, L.

submitted to the EMBL Data Library, December 1996

A:Description: The sequence of C. elegans cosmid T01B11.

A:Reference number: Z20099

A:Accession: T25850

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-313 <GRI>

A:Cross-references: EMBL: U80931; PIDN: AAB38001.1; GSPDB: GN00022; CESP: T01B11.4

A:Experimental source: strain Bristol N2; clone T01B11

C:Genetics:

A:Gene: CESP:T01B11.4

A:Map position: 4

A:Introns: 4/1, 191/2

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 67.3%; Score 1039; DB 2; Length 313;  
Best Local Similarity 70.9%; Pred. No. 2.6e-84;

Matches 207; Conservative 29; Mismatches 52; Indels 4; Gaps 3;

QY 8 FAKDFLAGIAAISTAVAPIERVKLLQVOHASKQIADKQYKIVICI 67  
DB 25 FLIDLASGTAASAASKTAVAPIERVKLLQVOHASKQIADKQYKIVICI 84  
QY 68 LSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLAGGAAGTS 127  
DB 85 AALMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLAGGAAGTS 144  
QY 128 LCFVYPLDFAFRTLAADVKGSGTEREFGDCLVYKITSDDGIRGYOGFSVSGIITV 187  
DB 145 LCFVYPLDFAFRTLAADVKGSGTEREFGDCLVYKITSDDGIRGYOGFSVSGIITV 203  
QY 188 RAAVFGVDTAKGMLPDPKNTHTVSWMTAQVTVAVAGVSYPTVRRRMQSGRKG 246  
DB 204 RAAVFGVDTAKGMLPDPKNTHTVSWMTAQVTVAVAGVSYPTVRRRMQSGRKG 262  
QY 247 ADIMYTGTVDCWRKIFRDEGSKAFKFGKAMSNTLRGMAFVLVLYDELKXYI 298  
DB 263 -DVLYKNTLDCAVKITRDEGSKAFKFGKAMSNTLRGMAFVLVLYDELKXYI 313

# RESULT 12

T25371

hypochemical protein T27B9.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 11-Jan-2000

C:Accession: T25371

R:Liloyd, C.  
submitted to the EMBL Data Library, November 1996

A:Reference number: Z20024

A:Accession: T25371

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-300 <Wtl>

A:Cross-references: EMBL: Z82059; PIDN: CAB04874.1; GSPDB: GN00021; CESP: T27B9.1

A:Experimental source: clone T27B9

C:Genetics:

A:Gene: CESP:T27B9.1

A:Map position: 3

A:Introns: 20/1, 41/3, 115/2

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 67.3%; Score 1036; DB 2; Length 300;  
Best Local Similarity 69.2%; Pred. No. 3e-84;  
Matches 202; Conservative 37; Mismatches 49; Indels 4; Gaps 3;



Db 8 NPAADFLMGISAIKTVVPIERVKMLIOTODSIPEIKSGOVERYSGLINCERVSKE 67  
 Qy 65 QGVLSFMRGNLANVIRYFPTQALNFAFKDKYQIFLAGVDKHTQFMRYFAGNLASGGAAG 124  
 Db 68 QGVLSMRGNVANVIRYFPTQALNFAFKDYFNIF-PRYDQNTDPSKEFCVNILSGATAG 126  
 Qy 125 ATSLCEVYPLDPARTRLADVKGSGTEREFRLGDCLVKITKSDGIRGLYOGFSVVOGI 184  
 Db 127 AISLILIVYPLDPARTRLASDICK-GKDRQFTGLFDCLAKIYKQTGLSLYSGFVSVTGI 185  
 Qy 185 IIRPAAYFCVYDTAKML-PDBKNTIYVSMIAQYTAVAGVSYPPDYVRRRMMMSG 243  
 Db 186 IYRGSYFGLYDSAKALLFTNDKNTNIVLKWAVAQSVTILAGLISYPPDYVRRRMMMSG 245  
 Qy 244 RKG-ADIMYTGTVDCMRKIFRDEGSKAFPGKAMSNVLRGMGAFVLYLDELKXVI 298  
 Db 246 RKGKEIQYKNTIDCMIKILRNEGKFGPKGAMNAVIRGAGALVLFYDELQKLI 301

Search completed: December 18, 2003, 17:11:23  
 Job time : 21 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 18, 2003, 17:07:54 / Search time 41 Seconds  
(without alignments)  
1875.602 Million cell updates/sec

Title: US-09-185-904A-33  
Perfect score: 1543  
Sequence: 1 MTEQALSFAPKDFLAGIAAA.....LRGNGAFVLVDELKKVI 298

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPTREMBL\_23.\*  
2: sp\_archaea.\*  
3: sp\_bacteria.\*  
4: sp\_fungi.\*  
5: sp\_human.\*  
6: sp\_invertebrate.\*  
7: sp\_mammal.\*  
8: sp\_mhc.\*  
9: sp\_organelle.\*  
10: sp\_plant.\*  
11: sp\_prodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacterioph.\*  
17: sp\_archaeop.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1474	95.5	298	13 Q8AYM3	Q8aym3 gallus gall
2	1451	94.0	298	6 Q8SQH5	Q8sqh5 bos taurus
3	1446	93.7	298	13 Q8JH10	Q8jh10 brachydanio
4	1422	92.2	298	6 O46373	O46373 oryctolagus
5	1421	92.1	298	13 Q919M9	Q919m9 xenopus lae
6	1414	91.6	298	11 Q8BVI9	Q8bvi9 mus musculu
7	1409	91.3	298	13 Q9PRH1	Q9prh1 rana rugosa
8	1406	91.1	298	13 Q9PRH2	Q9prh2 rana rugosa
9	1402	90.9	299	5 Q95VX4	Q95vx4 ethiostigm
10	1300	84.3	317	13 Q91336	Q91336 rana sylvat
11	1259	81.6	300	5 Q9NHWS	Q9nhws lucilia cup
12	1254.5	81.3	300	5 Q9NHWS	Q9nhws lucilia cup
13	1235.5	80.1	288	5 O44093	O44093 drosophila
14	1187.5	76.7	288	5 O44094	O44094 drosophila
15	1183.5	76.2	304	5 Q25129	Q25129 halocynthia
16	1176.5	76.2	304	5 Q25129	Q25129 halocynthia

17	1159	75.1	254	11 Q8BK05	Q8bk05 mus musculu
18	1137.5	73.7	307	5 O62526	O62526 drosophila
19	1119	72.5	315	4 Q9H0C2	Q9h0c2 homo sapien
20	1041	67.5	313	5 Q21103	Q21103 caenorhabdi
21	1039	67.3	313	5 P91410	P91410 caenorhabdi
22	1038	67.3	300	5 O45865	O45865 caenorhabdi
23	1036.5	67.2	310	10 Q8H727	Q8h727 phycophor
24	996	64.5	309	5 Q97470	Q97470 dictyosteli
25	993.5	64.4	300	5 O01813	O01813 caenorhabdi
26	993	64.4	300	5 Q17407	Q17407 caenorhabdi
27	973.5	63.1	318	5 Q9B036	Q9b036 toxoplasma
28	947	61.4	307	5 Q81J34	Q81j34 plasmodium
29	946.5	61.3	307	8 Q9XM22	Q9xm22 ascaris suu
30	944	61.2	301	5 Q25692	Q25692 plasmodium
31	944	61.2	301	5 Q8MVR4	Q8mvr4 euptotes sp
32	943	61.1	301	5 Q26006	Q26006 plasmodium
33	936	60.7	308	5 Q8MVR7	Q8mvr7 nyctotherus
34	932	60.4	308	5 Q8MVR8	Q8mvr8 nyctotherus
35	924	59.9	306	5 Q8MVR5	Q8mvr5 nyctotherus
36	924	59.9	308	5 Q8MVR6	Q8mvr6 nyctotherus
37	827	53.6	170	6 Q9XS69	Q9xs69 sus scrofa
38	778.5	50.5	305	3 Q9P8M1	Q9p8m1 yarrowia li
39	767.5	49.7	302	3 Q8J0M2	Q8j0m2 yarrowia li
40	764	49.5	326	5 P91270	P91270 caenorhabdi
41	760	49.3	307	5 Q76286	Q76286 trypanosoma
42	759	49.2	303	3 Q74260	Q74260 candida par
43	756.5	49.0	305	5 Q18683	Q18683 caenorhabdi
44	753	48.8	307	5 Q26697	Q26697 trypanosoma
45	749	48.5	315	3 Q8J0U1	Q8j0u1 gaeananomy

ALIGNMENTS

RESULT 1  
ID Q8AYM3 PRELIMINARY; PRT; 298 AA.  
AC Q8AYM3;  
DT 01-MAR-2003 (TRENBLREL\_23, Created)  
DT 01-MAR-2003 (TRENBLREL\_23, Last sequence update)  
DE 01-MAR-2003 (TRENBLREL\_23, Last annotation update)  
DE ATP/ADP antiporter.  
GN AVANT.  
OS Gallus Gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Toyomizu M., Ueda M., Sato S., Seki Y., Sato K., Akiba Y.;  
RT "Cold-induced mitochondrial uncoupling and expression of chicken UCP  
RL and ANT mRNA in chicken skeletal muscle.";  
RL EMBL Lett. 0-0-0(2002).  
DR EMBL; AB068686; BAC15533.1; .  
SQ SEQUENCE 298 AA; 32847 MW; 1174C5BEC400A10D CRC64;

QY	Query Match	95.5%	Score 1474;	DB 13;	Length 298;
DB	Best Local Similarity	93.0%;	Pred. No. 2.5e-125;		
	Matches 277;	Conservative 14;	Mismatches 7;	Indels 0;	Gaps 0;
QY	1	MTEQALSFAPKDFLAGIAAISKRAVPIERVKLLLOVQASKOIADKQYGVDCIVR	60		
DB	1	MADDAISFLKDFLRGVAAAIISKRAVPIERVKLLLOVQASKOIADKQYGVDCIVR	60		
QY	61	IPKEQVLSEFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFRYFAGNIASG	120		
DB	61	IPKEQVLSEFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFRYFAGNIASG	120		
QY	121	GAAGATSLCEVYPLDFAFRTIADVDGKAGADREPSGIGDCLVIVITKSGDGLGYOGPNVS	180		
DB	121	GAAGATSLCEVYPLDFAFRTIADVDGKAGADREPSGIGDCLVIVITKSGDGLGYOGPNVS	180		

```

QY 181 VGGIIIRAYAFGVYDTAKGMLPDPKNTHTIVSWMIAGTAVAGVSYPPDTRRRMM 240
DB 181 VGGIIIRAYAFGVYDTAKGMLPDPKNTHTIVSWMIAGTAVAGVSYPPDTRRRMM 240
QY 241 QSGRKGADIMYGTGVCWKRIFRDEGKAPFKGAMSNVLRMGGAFLVLYDELKXYI 298
DB 241 QSGRKGADIMYGTGVCWKRIFRDEGKAPFKGAMSNVLRMGGAFLVLYDELKXYI 298

RESULT 2
ID 08SOH5 PRELIMINARY; PRT; 298 AA.
AC 08SOH5;
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Adenine nucleotide translocator 2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamazaki N., Shinohara Y., Tanida K., Terada H.;
RT "Structural properties of mammalian mitochondrial ADP/ATP carriers:
RT identification of possible amino acids that determine functional
RT differences in its isoforms."
RL Mitochondrion 1:371-379(2002).
EMBL; AB065433; BAB84673.1; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_car; 3.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
SQ SEQUENCE 298 AA; 32955 MW; CB6897BB987B79C0 CRC64;

Query Match 94.0%; Score 1451; DB 6; Length 298;
Best Local Similarity 92.2%; Pred. No. 3e-123;
Matches 273; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTEQATSPADPLAGIAAISTKAVAPIERVLLQVHASKQIADKQKGVDCIVR 60
DB 1 MTEQATSPADPLAGIAAISTKAVAPIERVLLQVHASKQIADKQKGVDCIVR 60
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDPAFRTLRADLVGKSGTEREFRLGDCLVKITSKGIRGLYQGFVS 180
DB 121 GAAGATSLCFVYPLDPAFRTLRADLVGKSGTEREFRLGDCLVKITSKGIRGLYQGFVS 180
QY 181 VGGIIIRAYAFGVYDTAKGMLPDPKNTHTIVSWMIAGTAVAGVSYPPDTRRRMM 240
DB 181 VGGIIIRAYAFGVYDTAKGMLPDPKNTHTIVSWMIAGTAVAGVSYPPDTRRRMM 240
QY 241 QSGRKGADIMYGTGVCWKRIFRDEGKAPFKGAMSNVLRMGGAFLVLYDELKXYI 296
DB 241 QSGRKGADIMYGTGVCWKRIFRDEGKAPFKGAMSNVLRMGGAFLVLYDELKXYI 296

RESULT 3
ID 08JHT0 PRELIMINARY; PRT; 298 AA.
AC 08JHT0;
DT 01-OCT-2002 (TEMBLrel. 22, Created)
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Solute carrier family 25 member 5 protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.

```

```

OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22035902; PubMed=12006978;
RA Golling G., Amsterdam A., Sun Z., Antonelli M., Maldonado E., Chen W.,
RA Burgess S., Haldi M., Artzt K., Farrington S., Lin S.-Y., Nissen R.M.,
RA Hopkins N.;
RT "Insertional mutagenesis in zebrafish rapidly identifies genes
RT essential for early vertebrate development."
RL Nat. Genet. 31:135-140(2002).
DR EMBL; AF506216; AAM3460.1; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR InterPro; IPR002030; Mit_uncoupling.
DR Pfam; PF00153; mito_car; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
SQ SEQUENCE 298 AA; 32763 MW; D78663CF65C51D39 CRC64;

Query Match 93.7%; Score 1446; DB 13; Length 298;
Best Local Similarity 91.9%; Pred. No. 8.5e-123;
Matches 274; Conservative 15; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQATSPADPLAGIAAISTKAVAPIERVLLQVHASKQIADKQKGVDCIVR 60
DB 1 MTEQATSPADPLAGIAAISTKAVAPIERVLLQVHASKQIADKQKGVDCIVR 60
QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120
DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDPAFRTLRADLVGKSGTEREFRLGDCLVKITSKGIRGLYQGFVS 180
DB 121 GAAGATSLCFVYPLDPAFRTLRADLVGKSGTEREFRLGDCLVKITSKGIRGLYQGFVS 180
QY 181 VGGIIIRAYAFGVYDTAKGMLPDPKNTHTIVSWMIAGTAVAGVSYPPDTRRRMM 240
DB 181 VGGIIIRAYAFGVYDTAKGMLPDPKNTHTIVSWMIAGTAVAGVSYPPDTRRRMM 240
QY 241 QSGRKGADIMYGTGVCWKRIFRDEGKAPFKGAMSNVLRMGGAFLVLYDELKXYI 298
DB 241 QSGRKGADIMYGTGVCWKRIFRDEGKAPFKGAMSNVLRMGGAFLVLYDELKXYI 298

RESULT 4
ID 046373 PRELIMINARY; PRT; 298 AA.
AC 046373;
DT 01-JUN-1998 (TEMBLrel. 06, Created)
DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Yamaguchi N., Kasai M.;
RT "Identification of a 30kDa calsequestrin-binding protein, which
RT regulates calcium release from sarcoplasmic reticulum of rabbit
RT skeletal muscle."
RL J. Biochem. 335:541-547(1998).
CC - - SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB009386; BAA23777.1; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR InterPro; IPR002030; Mit_uncoupling.
DR Pfam; PF00153; mito_car; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.

```



DR PROSITE, PS00215; MITOCH\_CARRIER, 3.  
 KW Membrane; Transmembrane; Transport.  
 SQ SEQUENCE 298 AA; 32901 MW; CAEA32C88164AD78 CRC64;

Query Match 92.2%; Score 1422; DB 6; Length 298;  
 Best Local Similarity 88.9%; Pred. No. 1.3e-120;  
 Matches 265; Conservative 20; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGGIAAISKTAIVAPIERVKLLQVQHASKOIAADKQYKGIIVDCIVR 60  
 DB 1 MSDQALSLKDFLAGGVAASVKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVRR 60  
 QY 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVGHQTFWRYPAGNLSG 120  
 DB 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVGHQTFWRYPAGNLSG 120  
 QY 121 GAAGATSLCFYVPLDPARTRLAADVGKSTEREFGDGLCVKITSKGIRGLYGFSSVS 180  
 DB 121 GAAGATSLCFYVPLDPARTRLAADVGKAAOREFGDGLCVKITSKGIRGLYGFSSVS 180  
 QY 181 VGGIIIRAAAFGVYDTRAKGMLPDPKNTHTIVSWMIAQTVAVAGVSYPPDYRRRRMM 240  
 DB 181 VGGIIIRAAAFGVYDTRAKGMLPDPKNTHTIVSWMIAQTVAVAGVSYPPDYRRRRMM 240  
 QY 241 OSGRKADIMYTGIVDCWKRKIFRDEGGAFFKGAWSNVLRMGGAFLVLYDELKCVI 298  
 DB 241 OSGRKADIMYTGIVDCWKRKIAKDEGAKAFKGAWSNVLRMGGAFLVLYDELKCVI 298

RESULT 5

QY 0919M9 PRELIMINARY; PRT; 298 AA.  
 AC 0919M9;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Adenine nucleotide translocase.  
 GN ANTI.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Crawford M.J., Khosrowshahian F., Varmura S.L., Liverage R.A.;  
 RT "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and  
 Dynamic Patterns of Expression During Development.";  
 RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 DR EMBL: AF231347; AAF63471.1;  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR InterPro; IPR002067; Mit\_carrier.  
 DR InterPro; IPR002030; Mit\_uncoupling.  
 DR Pfam; PF00153; mito\_carr; 3.  
 DR PRINTS; PRO0926; MITOCARRIER.  
 DR PRINTS; PRO0784; MTUNCOUPLING.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KW Membrane; Transmembrane; Transport.  
 SQ SEQUENCE 298 AA; 32940 MW; 91B740133751877F CRC64;

Query Match 92.1%; Score 1421; DB 13; Length 298;  
 Best Local Similarity 90.3%; Pred. No. 1.6e-120;  
 Matches 269; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGGIAAISKTAIVAPIERVKLLQVQHASKOIAADKQYKGIIVDCIVR 60  
 DB 1 MTEQAISFAKDFLAGGIAAISKTAIVAPIERVKLLQVQHASKOITADKHKGIIDCVRR 60  
 QY 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVGHQTFWRYPAGNLSG 120  
 DB 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVGHQTFWRYPAGNLSG 120

QY 121 GAAGATSLCFYVPLDPARTRLAADVGKSTEREFGDGLCVKITSKGIRGLYGFSSVS 180  
 DB 121 GAAGATSLCFYVPLDPARTRLAADVGKAAOREFGDGLCVKITSKGIRGLYGFSSVS 180  
 QY 181 VGGIIIRAAAFGVYDTRAKGMLPDPKNTHTIVSWMIAQTVAVAGVSYPPDYRRRRMM 240  
 DB 181 VGGIIIRAAAFGVYDTRAKGMLPDPKNTHTIVSWMIAQTVAVAGVSYPPDYRRRRMM 240  
 QY 241 OSGRKADIMYTGIVDCWKRKIFRDEGGAFFKGAWSNVLRMGGAFLVLYDELKCVI 298  
 DB 241 OSGRKADIMYTGIVDCWKRKIAKDEGGAFFKGAWSNVLRMGGAFLVLYDELKCVI 298

RESULT 6

QY 09BVI9 PRELIMINARY; PRT; 298 AA.  
 AC 09BVI9;  
 DT 01-MAR-2003 (Tremblrel. 23, Created)  
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE Solute carrier family 25.  
 OS Mus musculus (mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK078077; BAC37117.1;  
 SQ SEQUENCE 298 AA; 32904 MW; F94C89009836710B CRC64;

Query Match 91.6%; Score 1414; DB 11; Length 298;  
 Best Local Similarity 88.6%; Pred. No. 6.8e-120;  
 Matches 264; Conservative 20; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGGIAAISKTAIVAPIERVKLLQVQHASKOIAADKQYKGIIVDCIVR 60  
 DB 1 MGRKALSLKDFLAGGIAAASVKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVRR 60  
 QY 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVGHQTFWRYPAGNLSG 120  
 DB 61 IPKEQGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVGHQTFWRYPAGNLSG 120  
 QY 121 GAAGATSLCFYVPLDPARTRLAADVGKSTEREFGDGLCVKITSKGIRGLYGFSSVS 180  
 DB 121 GAAGATSLCFYVPLDPARTRLAADVGKSSQREFGDGLCVKITSKGIRGLYGFSSVS 180  
 QY 181 VGGIIIRAAAFGVYDTRAKGMLPDPKNTHTIVSWMIAQTVAVAGVSYPPDYRRRRMM 240  
 DB 181 VGGIIIRAAAFGVYDTRAKGMLPDPKNTHTIVSWMIAQSTVAVAGVSYPPDYRRRRMM 240  
 QY 241 OSGRKADIMYTGIVDCWKRKIFRDEGGAFFKGAWSNVLRMGGAFLVLYDELKCVI 298  
 DB 241 OSGRKADIMYTGIVDCWKRKIAKDEGANAFKGAWSNVLRMGGAFLVLYDELKCVI 298

RESULT 7

QY 09PRH1 PRELIMINARY; PRT; 298 AA.  
 AC 09PRH1;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
 DE ADP/ATP translocase.  
 OS Rana rugosa (wrinkled frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

OX NCBI\_TaxID=8410;  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=9083429; PubMed=9866197;  
 RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;  
 RT "The origin and differentiation of the heteromorphic sex chromosomes  
 RT Z, W, X, and Y in the frog *Rana rugosa*, inferred from the sequences of  
 RT a sex-linked gene, ADP/ATP translocase.";  
 RL Mol. Biol. Evol. 15:1612-1619(1998).  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 DR EMBL: AB008463; BAA36513.1; -;  
 DR EMBL: AB008456; BAA36506.1; -;  
 DR EMBL: AB008461; BAA36511.1; -;  
 DR EMBL: AB008462; BAA36512.1; -;  
 DR InterPro: IPR001993; Mitochondrion carrier.  
 DR InterPro: IPR002067; Mitochondrion carrier.  
 DR InterPro: IPR002030; Mitochondrion carrier.  
 DR Pfam: PF00153; mito\_carrier\_3.  
 DR PRINTS: PR00926; MITOCARRIER.  
 DR PRINTS: PR00784; MTUNCOUPLING.  
 DR PROSITE: PS00215; MITOCH\_CARRIER.  
 KM Membrane; Transmembrane; Transport.  
 SQ SEQUENCE 298 AA; 33054 MW; B0E23AD56F548D36 CRC64;  
 Query Match 91.3%; Score 1409; DB 13; Length 298;  
 Best Local Similarity 88.6%; Pred. No. 1.9e-119;  
 Matches 26; Conservative 19; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 MTEOAI SFADPLAGIAAISTAVAPIERVKLLLOVHASQIADKQYKGIIVDCIVR 60  
 DB 1 MTPAASIFADPLAGIAAISTAVAPIERVKLLLOVHASQIADKQYKGIIVDCIVR 60  
 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRFAGNLASG 120  
 DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDFARTRLAADVGSGEREFGDGLVKTSDGIRGLYQGFVS 180  
 DB 121 GAAGATSLCFVYPLDFARTRLAADVGSGEREFGDGLVKTSDGIRGLYQGFVS 180  
 QY 181 VGGIIRYRAVFGVYDTAKGMLPDPKNTHTVSWMTAQVTAVAGVSYPTVRRMM 240  
 DB 181 VGGIIRYRAVFGVYDTAKGMLPDPKNTHTVSWMTAQVTAVAGVSYPTVRRMM 240  
 QY 241 QSGRKADIMYTGVDCWKIFRDEGKAFKFGKAMSNVLKMGCAFVLVYDELKXYI 298  
 DB 241 QSGRKADIMYTGVDCWKIFRDEGKAFKFGKAMSNVLKMGCAFVLVYDELKXYI 298  
 RESULT 8  
 Q9PRH2 PRELIMINARY; PRT; 298 AA.  
 AC Q9PRH2;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE ADP/ATP translocase.  
 OS *Rana rugosa* (Wrinkled frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
 NCBI\_TaxID=8410;  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=9083429; PubMed=9866197;  
 RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;  
 RT "The origin and differentiation of the heteromorphic sex chromosomes  
 RT Z, W, X, and Y in the frog *Rana rugosa*, inferred from the sequences of  
 RT a sex-linked gene, ADP/ATP translocase.";  
 RL Mol. Biol. Evol. 15:1612-1619(1998).  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 DR EMBL: AB008460; BAA36510.1; -;  
 DR EMBL: AB008458; BAA36508.1; -;  
 DR EMBL: AB008459; BAA36509.1; -;

DR InterPro: IPR001993; Mitochondrion carrier.  
 DR InterPro: IPR002067; Mitochondrion carrier.  
 DR InterPro: IPR002030; Mitochondrion carrier.  
 DR Pfam: PF00153; mito\_carrier\_3.  
 DR PRINTS: PR00926; MITOCARRIER.  
 DR PRINTS: PR00784; MTUNCOUPLING.  
 DR PROSITE: PS00215; MITOCH\_CARRIER.  
 KM Membrane; Transmembrane; Transport.  
 SQ SEQUENCE 298 AA; 33082 MW; B0E225B867599A06 CRC64;  
 Query Match 91.1%; Score 1406; DB 13; Length 298;  
 Best Local Similarity 88.3%; Pred. No. 3.6e-119;  
 Matches 26; Conservative 20; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 MTEOAI SFADPLAGIAAISTAVAPIERVKLLLOVHASQIADKQYKGIIVDCIVR 60  
 DB 1 MTPAASIFADPLAGIAAISTAVAPIERVKLLLOVHASQIADKQYKGIIVDCIVR 60  
 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRFAGNLASG 120  
 DB 61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDFARTRLAADVGSGEREFGDGLVKTSDGIRGLYQGFVS 180  
 DB 121 GAAGATSLCFVYPLDFARTRLAADVGSGEREFGDGLVKTSDGIRGLYQGFVS 180  
 QY 181 VGGIIRYRAVFGVYDTAKGMLPDPKNTHTVSWMTAQVTAVAGVSYPTVRRMM 240  
 DB 181 VGGIIRYRAVFGVYDTAKGMLPDPKNTHTVSWMTAQVTAVAGVSYPTVRRMM 240  
 QY 241 QSGRKADIMYTGVDCWKIFRDEGKAFKFGKAMSNVLKMGCAFVLVYDELKXYI 298  
 DB 241 QSGRKADIMYTGVDCWKIFRDEGKAFKFGKAMSNVLKMGCAFVLVYDELKXYI 298  
 RESULT 9  
 Q9YIC4 PRELIMINARY; PRT; 298 AA.  
 AC Q9YIC4;  
 DT 01-MAY-1999 (TREMBlrel. 10, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE ADP/ATP translocase.  
 OS *Rana rugosa* (Wrinkled frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
 NCBI\_TaxID=8410;  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=9083429; PubMed=9866197;  
 RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;  
 RT "The origin and differentiation of the heteromorphic sex chromosomes  
 RT Z, W, X, and Y in the frog *Rana rugosa*, inferred from the sequences of  
 RT a sex-linked gene, ADP/ATP translocase.";  
 RL Mol. Biol. Evol. 15:1612-1619(1998).  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 DR EMBL: AB008457; BAA36507.1; -;  
 DR InterPro: IPR001993; Mitochondrion carrier.  
 DR InterPro: IPR002067; Mitochondrion carrier.  
 DR InterPro: IPR002030; Mitochondrion carrier.  
 DR Pfam: PF00153; mito\_carrier\_3.  
 DR PRINTS: PR00926; MITOCARRIER.  
 DR PRINTS: PR00784; MTUNCOUPLING.  
 DR PROSITE: PS00215; MITOCH\_CARRIER.  
 KM Membrane; Transmembrane; Transport.  
 SQ SEQUENCE 298 AA; 33068 MW; 15B270BD37099A00 CRC64;  
 Query Match 90.9%; Score 1402; DB 13; Length 298;  
 Best Local Similarity 87.9%; Pred. No. 8.3e-119;  
 Matches 26; Conservative 21; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 MTEOAI SFADPLAGIAAISTAVAPIERVKLLLOVHASQIADKQYKGIIVDCIVR 60

```

Db      1 MTDAAISFADKDFLAGGVAASIKTAVALPIERVKLLLOVQHASKQITADKQYKIMDCVVR 60
Qy      1 IPEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDHGTQFWRFPAGNLASG 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 IPEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLDVNDKRTQFWRFPAGNLASG 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      121 GAAGATSLCFYVPLDPARTRLAADVKGSGTEREFGDLGDKLVKITSQDGRGLYQGFVS 180
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 GAAGATSLCFYVPLDPARTRLAADVKGADREFGDLGDKLVKITSQDGRGLYQGFVS 180
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      181 VGGIITRAAYFGVYDTRAKGMLPDPKNTHTIVSMIAQTVAAGVSYPPDTRRRMM 240
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 VGGIITRAAYFGVYDTRAKGMLPDPKNTHTIVSMIAQSVTAAGVSYPPDTRRRMM 240
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      241 QSGRKADIMYTGVDKCRKIFRDEGKAFKFGKAMSNLRGKGFVLVLDLKKVI 298
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 QSGRKADIMYTGVDKCRKIFRDEGKAFKFGKAMSNLRGKGFVLVLDLKKVI 298
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
Q95VX4 PRELIMINARY; PRT; 299 AA.
ID      095VX4
AC      Q95VX4;
DT      01-DEC-2001 (Tremblrel. 19, Created)
DT      01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT      01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE      ADP-ATP translocase.
OS      Ethmostigmus rubripes.
OC      Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;
OC      Pleurostigmophora; Scolopendromorpha; Scolopendridae; Ethmostigmus.
OX      NCBI_TaxID=62613;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Burnell J.N.;
RT      "Nucleotide sequence of an ADP-ATP translocator of Ethmostigmus
RT      rubripes."
RL      Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR      EMBL; AF401758; AAL02100.1; -.
DR      InterPro; IPR001993; Mitoch_carrier.
DR      InterPro; IPR002067; Mit_carrier.
DR      Pfam; PF00153; mito_carrier; 3.
DR      PRINTS; PR00926; MITOCARRIER.
DR      PROSITE; PS00215; MITOCH_CARRIER; 3.
SQ      SEQUENCE 299 AA; 33037 MW; 3C3BCB26F7C3C5E CRC64;

Query Match      84.3%; Score 1300; DB 5; Length 299;
Best Local Similarity 81.5%; Pred. No. 1.5e-109;
Matches 243; Conservative 26; Mismatches 29; Indels 0; Gaps 0;

Qy      1 MTEOAI SFADKDFLAGGIAAASIKTAVALPIERVKLLLOVQHASKQITADKQYKIMDCVVR 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MTDAAISFADKDFLAGGVAASIKTAVALPIERVKLLLOVQHASKQITADKQYKIMDCVVR 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      61 IPEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDHGTQFWRFPAGNLASG 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 IPEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLDVNDKRTQFWRFPAGNLASG 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      121 GAAGATSLCFYVPLDPARTRLAADVKGSGTEREFGDLGDKLVKITSQDGRGLYQGFVS 180
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 GAAGATSLCFYVPLDPARTRLAADVKGADREFGDLGDKLVKITSQDGRGLYQGFVS 180
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      181 VGGIITRAAYFGVYDTRAKGMLPDPKNTHTIVSMIAQTVAAGVSYPPDTRRRMM 240
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 VGGIITRAAYFGVYDTRAKGMLPDPKNTHTIVSMIAQSVTAAGVSYPPDTRRRMM 240
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      241 QSGRKADIMYTGVDKCRKIFRDEGKAFKFGKAMSNLRGKGFVLVLDLKKVI 298
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 QSGRKADIMYTGVDKCRKIFRDEGKAFKFGKAMSNLRGKGFVLVLDLKKVI 298
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
Q91336 PRELIMINARY; PRT; 317 AA.
ID      Q91336

```

```

AC      Q91336;
DT      01-NOV-1996 (Tremblrel. 01, Created)
DT      01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT      01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE      ADP/ATP translocase.
OS      Rana sylvatica (wood frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX      NCBI_TaxID=45438;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Tissue=Liver;
RC      MEDLINE=97398141; PubMed=9256066;
RX      Cai Q., Greenway S.C., Storey K.B.;
RA      "Differential regulation of the mitochondrial ADP/ATP translocase gene
RT      in wood frogs under freezing stress."
RL      Biochim. Biophys. Acta 1353:69-78 (1997).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Tissue=Liver;
RC      Cai Q., Storey K.B.;
RL      Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.
CC      -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR      EMBL; U44832; AAA97882.2; -.
DR      InterPro; IPR001993; Mitoch_carrier.
DR      InterPro; IPR002067; Mit_carrier.
DR      Pfam; PF00153; mito_carrier; 3.
DR      PRINTS; PR00926; MITOCARRIER.
DR      PROSITE; PS00215; MITOCH_CARRIER; 3.
KW      Membrane; Transmembrane; Transport.
SQ      SEQUENCE 317 AA; 35005 MW; 5F66B7ED8D5CEB72 CRC64;

Query Match      81.6%; Score 1259; DB 13; Length 317;
Best Local Similarity 86.8%; Pred. No. 8.2e-106;
Matches 236; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

Qy      1 MTEOAI SFADKDFLAGGIAAASIKTAVALPIERVKLLLOVQHASKQITADKQYKIMDCVVR 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MTDAAISFADKDFLAGGVAASIKTAVALPIERVKLLLOVQHASKQITADKQYKIMDCVVR 60
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      61 IPEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDHGTQFWRFPAGNLASG 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 IPEQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLDVNDKRTQFWRFPAGNLASG 120
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      121 GAAGATSLCFYVPLDPARTRLAADVKGSGTEREFGDLGDKLVKITSQDGRGLYQGFVS 180
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 GAAGATSLCFYVPLDPARTRLAADVKGADREFGDLGDKLVKITSQDGRGLYQGFVS 180
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      181 VGGIITRAAYFGVYDTRAKGMLPDPKNTHTIVSMIAQTVAAGVSYPPDTRRRMM 240
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 VGGIITRAAYFGVYDTRAKGMLPDPKNTHTIVSMIAQSVTAAGVSYPPDTRRRMM 240
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      241 QSGRKADIMYTGVDKCRKIFRDEGKAFKFGKAMSNLRGKGFVLVLDLKKVI 272
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 QSGRKADIMYTGVDKCRKIFRDEGKAFKFGKAMSNLRGKGFVLVLDLKKVI 272
        |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
Q81RAO PRELIMINARY; PRT; 312 AA.
ID      Q81RAO
AC      Q81RAO;
DT      01-MAR-2003 (Tremblrel. 23, Created)
DT      01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT      01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE      CG16944-PC.
GN      SE8B.
OS      Drosophila melanogaster (fruit fly).
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC      Ephydroidea; Drosophilidae; Drosophila.
OX      NCBI_TaxID=7227;
RN      [1]
RP      SEQUENCE FROM N.A.

```

RA MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Adamatis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,  
 RA Abril J.F., Ashgari A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballow R.M., Baau A.V., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,  
 RA Burks J.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA DePablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fodor C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibeigwe C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laoko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod W.P., McPherson D.,  
 RA Merkulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Turner C., Turner E., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,  
 RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*";  
 RL Science 287:2165-2195(2000).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RA Ceiniker S.E., Adams M.D., Krommler B., Wan K.H., Holt R.A.,  
 RA Evans C.A., Gocayne J.D., Adamatis P.G., Brandon R.C., Rogers Y.,  
 RA Banzon J., An H., Baldwin D., Beeson K.Y., Busam D.A.,  
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
 RA Dodson K., Doreet V., Dou P.L.E., Doyle C., Dreese D., Farfan D.,  
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,  
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
 RA Ibeigwe C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
 RA Paclob J., Paragas V., Park S., Patel S., Pfeiffer B.,  
 RA Phounavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,  
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
 RT "Sequencing of *Drosophila melanogaster* genome";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RP SEQUENCE FROM N.A.  
 RA Miera S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hradecky P., Huang Y., Kaminiker J.S., Prochnik S.E., Smith C.D.,  
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Ceiniker S.E.,  
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
 RA Krommler B., Marshall B., Millburn G., Richter J., Russo S.,  
 RA Seale S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,  
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
 RT "Annotation of *Drosophila melanogaster* genome";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RP SEQUENCE FROM N.A.  
 RA Adams M.D., Ceiniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 [5]  
 RP SEQUENCE FROM N.A.

RA flyBase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AE003484; AAN09267.1;  
 SQ SEQUENCE 312 AA; 34214 MW; 78D5834E748168DF CRC64;  
 Query Match 81.3%; Score 1254.5; DB 5; Length 312;  
 Best Local Similarity 80.6%; Pred. No. 2.1e-103;  
 Matches 237; Conservative 23; Mismatches 33; Indels 1; Gaps 1;  
 QY 5 AISEADPLAGGIAAISTKAVAPIERVKLLQVQHASQIOADKQYKGIIVDPIPKK 64  
 DB 20 AAGFVADPAGGISAASKTAAPIERVKLLQVQHASQIOADKQYKGIIVDPIPKK 79  
 QY 65 QGVLSFWRGKLANVIRFPFOALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLAGGAAG 124  
 DB 80 QGVSSFWRGKLANVIRFPFOALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLAGGAAG 139  
 QY 125 ATSLCTVYPLDPARTLADVGKSGTEREFGIGDCLVKTYSDDGIRGLYOGFSVSVOGI 184  
 DB 140 ATSLCTVYPLDPARTLADVGKSG-QREFTGLGNCLTKIKFSKDGIVGLYRGFVSVOGI 198  
 QY 185 IIRAAVPGYDPAKGMLDPPKTHIVSWMIAQVTAAGVSYPPDVRBRMMQSGR 244  
 DB 199 IIRAAVPGYDPAKGMLDPPKTHIVSWMIAQVTAAGVSYPPDVRBRMMQSGR 258  
 QY 245 KGADIVYTGIVDCMRKIFRDEGKAFKAGWSNVLRMGGAFLVLYDEIKKVI 298  
 DB 259 KAREVYVYKTHCMATIAKQEGTGAFFKGFASNLNGTGAFLVLYDEIKKVL 312  
 RESULT 13  
 ID Q9NHW5 PRELIMINARY; PRT; 300 AA.  
 AC Q9NHW5;  
 DT 01-OCT-2000 (TEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)  
 DE ADP/ATP translocase.  
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Calyptrata; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Lucilidae; Lucilia.  
 NC NCBI\_TaxID=7375;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SRRJN=SS mal seeking;  
 RA Chen Z., Fair J.A., Batterham P.;  
 RT "A cDNA clone encoding the ADP/ATP translocase of *Lucilia cuprina*,"  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 DR EMBL: AF218587; AAF32322.1; -  
 DR InterPro: IPR001993; Mitoch carrier.  
 DR InterPro: IPR002067; Mitc\_carrier.  
 DR Pfam: PF00153; mito\_car1.3.  
 DR PRINTS: PR00926; MITOCH\_CARRIER.  
 DR PROSITE: PS00215; MITOCH\_CARRIER.  
 KM Membrane; Transmembrane; Transport.  
 SQ SEQUENCE 300 AA; 33036 MW; 5459DFOEAD0E2B742 CRC64;  
 Query Match 80.1%; Score 1235.5; DB 5; Length 300;  
 Best Local Similarity 79.5%; Pred. No. 1e-103;  
 Matches 233; Conservative 24; Mismatches 35; Indels 1; Gaps 1;  
 QY 6 ISPAKDFLAGGIAAISTKAVAPIERVKLLQVQHASQIOADKQYKGIIVDPIPKK 65  
 DB 9 LGFVKDPFAGGISAASKTAAPIERVKLLQVQHASQIOADKQYKGIIVDPIPKK 68  
 QY 66 GVLSPFRGKLANVIRFPFOALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLAGGAAG 125  
 DB 69 GFLSPFRGKLANVIRFPFOALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLAGGAAG 128  
 QY 126 TSLCFVYPLDPARTLADVGKSGTEREFGIGDCLVKTYSDDGIRGLYOGFSVSVOGI 185

Db 129 TSLCFTVPLDEARTRLAADTKGQ-QREFTLGNCILAKI FKS DGLVGLYRGFVSGII 187  
 QY 186 IYRAAYFGVYDTAKGMLPDPKNTHTIVSWMIQOTVAVAGVSPEDTVRRMMMOGRK 245  
 Db 188 IYRAAYFGVYDTAKGMLPDPKNTHTIVSWMIQOTVAVAGVSPEDTVRRMMMOGRK 247  
 QY 246 GADIMYTGTVDCWKRI FRDEGKAFPKGAMSNVLRGMAFVLVYDELKVI 298  
 Db 248 ATEIITYKNTLHCWATIAKQEGTGAFFKGA FSNVLKGTGAFVLVYDEIKKFL 300

## RESULT 14

044093 PRELIMINARY; PRT; 288 AA.  
 ID 044093  
 AC 044093;  
 DT 01-JUN-1998 (TREMBLrel. 06, Last created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last annotation update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE ADP/ATP translocase (Fragment).  
 GN SE5B.  
 OS Drosophila pseudoobscura (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7237;  
 RP [1]  
 RN SEQUENCE FROM N.A.  
 RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;  
 RL Genetics 0:0-0(1997).  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 DR EMBL; AF025798; AAB87883.1; -.  
 DR FlyBase; FBgn0023292; Dpseb\seeb.  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR InterPro; IPR002067; Mlt\_carrier.  
 DR Pfam; PF00153; mito\_cartr; 3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KW Membrane; Repeat; Transmembrane; Transport.  
 FT \* NON TER  
 FT 288  
 SQ SEQUENCE 288 AA; 31725 MW; 052B0CC0050436B0 CRC64;

Query Match 77.0%; Score 1187.5; DB 5; Length 288;  
 Best Local Similarity 80.7%; Pred. No. 2.2e-99;  
 Matches 230; Conservative 19; Mismatches 33; Indels 3; Gaps 3;  
 QY 5 AISRKDLGAGIAAISKTAVAPIERVKLLQVQHASKQIADKQYGIYDCVIRIPKE 64  
 Db 7 AIGFKDFAAGISAAVSKTAVAPIERVKLLQVQHISKQISPDKQYKGMVDCFRIRIPE 66  
 QY 65 QGVLSFMRGNLANVIRYPTQALNPAFDKXKQIFLGVDKHTQFWRFAGNLSGGAAG 124  
 Db 67 QGFSSFMGNLANVIRYPTQALNPAFDKXKQIFLGVDKHTQFWRFAGNLSGGAAG 126  
 QY 125 ATSLCFVYPLDPARTRLADVGKSGTEREPRGLDCLVKITKSDGIRGLYOGFSVVOGI 184  
 Db 127 ATSLCFVYPLDPARTRLADVGKSG-QREFTLGNCILTKIFKSDGLVGLYRGFVSGOI 185  
 QY 185 IYRAAYFGVYDTAKGMLPDPKNTHTIVSWMIQOTVAVAGVSPEDTVRRMMMOGR 244  
 Db 186 IYRAAYFGVYDTAR-MLPDPKNTPIYISWAIACVTVAGIVSPEDTVRRMMMOGR 244  
 QY 245 KGADIMYTGTVDCWKRI FRDEGKAFPKGAMSNVLRGMAFVLV 289  
 Db 245 KATEIITYKNTLHCWATIAKQEGTGAFFKGA FSNVLKGTGAFVLV 288

## RESULT 15

044094 PRELIMINARY; PRT; 288 AA.  
 ID 044094  
 AC 044094;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE ADP/ATP translocase (Fragment).  
 GN SE5B.  
 OS Drosophila subobscura (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7241;  
 RP [1]  
 RN SEQUENCE FROM N.A.  
 RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;  
 RL Genetics 0:0-0(1997).  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
 DR EMBL; AF025799; AAB87884.1; -.  
 DR FlyBase; FBgn0023237; Dpseb\seeb.  
 DR InterPro; IPR001993; Mitoch\_carrier.  
 DR InterPro; IPR002067; Mlt\_carrier.  
 DR Pfam; PF00153; mito\_cartr; 3.  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KW Membrane; Repeat; Transmembrane; Transport.  
 FT \* NON TER  
 FT 288  
 SQ SEQUENCE 288 AA; 31775 MW; 06A1D1E477B81B26 CRC64;

Query Match 76.7%; Score 1183.5; DB 5; Length 288;  
 Best Local Similarity 80.4%; Pred. No. 5e-99;  
 Matches 229; Conservative 20; Mismatches 33; Indels 3; Gaps 3;  
 QY 5 AISRKDLGAGIAAISKTAVAPIERVKLLQVQHASKQIADKQYGIYDCVIRIPKE 64  
 Db 7 AMGFVKDFAAGISAAVSKTAVAPIERVKLLQVQHISKQISPDKQYKGMVDCFRIRIPE 66  
 QY 65 QGVLSFMRGNLANVIRYPTQALNPAFDKXKQIFLGVDKHTQFWRFAGNLSGGAAG 124  
 Db 67 QGFSSFMGNLANVIRYPTQALNPAFDKXKQIFLGVDKHTQFWRFAGNLSGGAAG 126  
 QY 125 ATSLCFVYPLDPARTRLADVGKSGTEREPRGLDCLVKITKSDGIRGLYOGFSVVOGI 184  
 Db 127 ATSLCFVYPLDPARTRLADVGKSG-QREFTLGNCILTKIFKSDGLVGLYRGFVSGOI 185  
 QY 185 IYRAAYFGVYDTAKGMLPDPKNTHTIVSWMIQOTVAVAGVSPEDTVRRMMMOGR 244  
 Db 186 IYRAAYFGVYDTAR-MLPDPKNTPIYISWAIACVTVAGIVSPEDTVRRMMMOGR 244  
 QY 245 KGADIMYTGTVDCWKRI FRDEGKAFPKGAMSNVLRGMAFVLV 289  
 Db 245 KATEIITYKNTLHCWATIAKQEGTGAFFKGA FSNVLKGTGAFVLV 288

Search completed: December 18, 2003, 17:09:58  
 Job time : 44 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 18, 2003, 17:10:04 ; Search time 31 Seconds  
(without alignments)  
1795.292 Million cell updates/sec

Title: US-09-185-904A-33  
Perfect score: 1543  
Sequence: 1 MTEQAISFAKDFLAGIAAA.....LRMGAFVLYDELKKVI 298

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues  
Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09D\_PUBCOMB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	298	US-09-811-094-33	Sequence 33, Appl
2	1543	100.0	298	US-09-810-644-33	Sequence 33, Appl
3	1543	100.0	298	US-09-185-904A-33	Sequence 33, Appl
4	1454	94.2	298	US-09-811-094-33	Sequence 32, Appl
5	1454	94.2	298	US-09-810-644-33	Sequence 32, Appl
6	1454	94.2	298	US-09-185-904A-32	Sequence 32, Appl
7	1385.5	89.8	297	US-09-811-094-31	Sequence 31, Appl
8	1385.5	89.8	297	US-09-810-644-31	Sequence 31, Appl
9	1385.5	89.8	297	US-09-185-904A-31	Sequence 31, Appl
10	811	52.6	179	US-10-029-386-32501	Sequence 32501, A
11	788.5	51.1	301	US-10-032-585-7194	Sequence 252, Ap
12	760.5	49.3	318	US-09-801-368-252	Sequence 170, App
13	749.5	48.6	386	US-09-734-569-170	Sequence 338, Ap
14	737	47.8	308	US-10-128-714-3338	Sequence 8338, Ap
15	737	47.8	308	US-10-128-714-8338	Sequence 8338, Ap

16	734.5	47.6	381	12	US-10-141-478A-2	Sequence 2, Appl
17	686	44.5	677	12	US-10-259-165-192	Sequence 192, App
18	518	33.6	132	9	US-09-925-301-1459	Sequence 1459, Ap
19	423	27.4	87	9	US-09-864-761-36440	Sequence 36440, A
20	368	23.8	475	10	US-09-777-921A-4	Sequence 4, Appl
21	368	23.8	477	10	US-09-777-921A-2	Sequence 2, Appl
22	333.5	21.6	410	10	US-09-777-921A-5	Sequence 5, Appl
23	326	21.1	384	12	US-10-094-749-1789	Sequence 1789, Ap
24	314	20.3	469	9	US-09-989-722-289	Sequence 289, App
25	314	20.3	469	9	US-09-989-723-289	Sequence 289, App
26	314	20.3	469	9	US-09-989-279-289	Sequence 289, App
27	314	20.3	469	9	US-09-989-727-289	Sequence 289, App
28	314	20.3	469	10	US-09-989-731-289	Sequence 289, App
29	314	20.3	469	10	US-09-989-732-289	Sequence 289, App
30	314	20.3	469	10	US-09-989-733-289	Sequence 289, App
31	314	20.3	469	10	US-09-989-734-289	Sequence 289, App
32	314	20.3	469	10	US-09-991-163-289	Sequence 289, App
33	314	20.3	469	10	US-09-993-604-289	Sequence 289, App
34	314	20.3	469	10	US-09-990-456-289	Sequence 289, App
35	314	20.3	469	10	US-09-989-721-289	Sequence 289, App
36	314	20.3	469	10	US-09-989-730-289	Sequence 289, App
37	314	20.3	469	10	US-09-989-732A-289	Sequence 289, App
38	314	20.3	469	10	US-09-989-735-289	Sequence 289, App
39	314	20.3	469	10	US-09-990-444-289	Sequence 289, App
40	314	20.3	469	10	US-09-991-181-289	Sequence 289, App
41	314	20.3	469	10	US-09-989-730-289	Sequence 289, App
42	314	20.3	469	10	US-09-990-436-289	Sequence 289, App
43	314	20.3	469	10	US-09-993-687-289	Sequence 289, App
44	314	20.3	469	11	US-09-989-734-289	Sequence 289, App
45	314	20.3	469	11	US-09-997-653-289	Sequence 289, App

## ALIGNMENTS

RESULT 1  
US-09-811-094-33  
Sequence 33, Application US/09811094  
Patent No. US2001004144A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, Christen M.  
APPLICANT: Davis, Robert E.  
APPLICANT: Clevenger, William  
APPLICANT: Wile, Sandra Eileen  
APPLICANT: Willet, Scott W.  
APPLICANT: Szabo, Tomas R.  
APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Moos, Walter H.  
APPLICANT: Pel, Yezhong  
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),  
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
FILE REFERENCE: 660088.420D4  
CURRENT FILING DATE: 2001-03-14  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 33  
LENGTH: 298  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-811-094-33

Query Match 100.0%; Score 1543; DB: 9; Length 298;  
Best Local Similarity 100.0%; Pred. No. 1e-156;  
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGIAAAISKTAFAPIREVKLLLOVQASKOIADKQYGVDCIVR 60  
DB 1 MTEQAISFAKDFLAGIAAAISKTAFAPIREVKLLLOVQASKOIADKQYGVDCIVR 60  
QY 61 IPKQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLSAG 120  
DB 61 IPKQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKHTQFMRYFAGNLSAG 120

```

QY      121 GAAGATSLCFVYPLDPARTRLAADVKGSGTEREFGDGLVKTSGDGRGLYOGFSVS 180
      |||
      121 GAAGATSLCFVYPLDPARTRLAADVKGSGTEREFGDGLVKTSGDGRGLYOGFSVS 180
Db      181 VOGIIIRAAVFGVYDTAKGMLPDPKXTHIVVSMIAQVTVAVAGVSYPEPTVRRMM 240
      |||
      181 VOGIIIRAAVFGVYDTAKGMLPDPKXTHIVVSMIAQVTVAVAGVSYPEPTVRRMM 240
Db      241 QSGRKGADIMYTGTVDCWKRIFRDEGSKAFPKGAMSNVLKMGGAFLVLYDELKKVI 298
      |||
      241 QSGRKGADIMYTGTVDCWKRIFRDEGSKAFPKGAMSNVLKMGGAFLVLYDELKKVI 298

```

# RESULT 2

```

US-09-810-644-33
; Sequence 33, Application US/09810644
; Patent No. US20020012992A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willet, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pei, Yazhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.420D3
; CURRENT APPLICATION NUMBER: US/09/810,644
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-810-644-33

```

Query Match 100.0%; Score 1543; DB 9; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 1e-156;  
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 MTEQALSFADFLAGGIAAIAISKTAAPIERVKLLQOVHASKOIADKQYKGIIVDCI 60
      |||
      1 MTEQALSFADFLAGGIAAIAISKTAAPIERVKLLQOVHASKOIADKQYKGIIVDCI 60
Db      61 IPKEQVLSFWRGNLANVIRYPTQALNFAFKQYKQIFLGVDKHTQFWRYPAGNLASG 120
      |||
      61 IPKEQVLSFWRGNLANVIRYPTQALNFAFKQYKQIFLGVDKHTQFWRYPAGNLASG 120
Db      121 GAAGATSLCFVYPLDPARTRLAADVKGSGTEREFGDGLVKTSGDGRGLYOGFSVS 180
      |||
      121 GAAGATSLCFVYPLDPARTRLAADVKGSGTEREFGDGLVKTSGDGRGLYOGFSVS 180
Db      121 GAAGATSLCFVYPLDPARTRLAADVKGSGTEREFGDGLVKTSGDGRGLYOGFSVS 180
QY      181 VOGIIIRAAVFGVYDTAKGMLPDPKXTHIVVSMIAQVTVAVAGVSYPEPTVRRMM 240
      |||
      181 VOGIIIRAAVFGVYDTAKGMLPDPKXTHIVVSMIAQVTVAVAGVSYPEPTVRRMM 240
Db      241 QSGRKGADIMYTGTVDCWKRIFRDEGSKAFPKGAMSNVLKMGGAFLVLYDELKKVI 298
      |||
      241 QSGRKGADIMYTGTVDCWKRIFRDEGSKAFPKGAMSNVLKMGGAFLVLYDELKKVI 298

```

# RESULT 3

```

US-09-185-904a-33
; Sequence 33, Application US/09185904A
; Patent No. US2002017185A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.

```

```

; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willet, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
; TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
; FILE REFERENCE: 660088.420
; CURRENT APPLICATION NUMBER: US/09/185,904A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-185-904a-33

```

Query Match 100.0%; Score 1543; DB 10; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 1e-156;  
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 MTEQALSFADFLAGGIAAIAISKTAAPIERVKLLQOVHASKOIADKQYKGIIVDCI 60
      |||
      1 MTEQALSFADFLAGGIAAIAISKTAAPIERVKLLQOVHASKOIADKQYKGIIVDCI 60
Db      61 IPKEQVLSFWRGNLANVIRYPTQALNFAFKQYKQIFLGVDKHTQFWRYPAGNLASG 120
      |||
      61 IPKEQVLSFWRGNLANVIRYPTQALNFAFKQYKQIFLGVDKHTQFWRYPAGNLASG 120
Db      121 GAAGATSLCFVYPLDPARTRLAADVKGSGTEREFGDGLVKTSGDGRGLYOGFSVS 180
      |||
      121 GAAGATSLCFVYPLDPARTRLAADVKGSGTEREFGDGLVKTSGDGRGLYOGFSVS 180
QY      181 VOGIIIRAAVFGVYDTAKGMLPDPKXTHIVVSMIAQVTVAVAGVSYPEPTVRRMM 240
      |||
      181 VOGIIIRAAVFGVYDTAKGMLPDPKXTHIVVSMIAQVTVAVAGVSYPEPTVRRMM 240
Db      241 QSGRKGADIMYTGTVDCWKRIFRDEGSKAFPKGAMSNVLKMGGAFLVLYDELKKVI 298
      |||
      241 QSGRKGADIMYTGTVDCWKRIFRDEGSKAFPKGAMSNVLKMGGAFLVLYDELKKVI 298

```

# RESULT 4

```

US-09-811-094-32
; Sequence 32, Application US/09811094
; Patent No. US20010044144A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willet, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pei, Yazhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/811,094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-094-32

```

Query Match 94.2%; Score 1454; DB 9; Length 298;  
 Best Local Similarity 92.6%; Pred. No. 3.5e-147;



Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Query 1 MTEOAIISFADPLAGIAAIAISKTAVAPIERVKLLLOVQHASKOITADKOKYKGIIDCVR 60  
 1 MTDALISFADPLAGIAAIAISKTAVAPIERVKLLLOVQHASKOITADKOKYKGIIDCVR 60  
 Db 1 MTDALISFADPLAGIAAIAISKTAVAPIERVKLLLOVQHASKOITADKOKYKGIIDCVR 60  
 Qy 1 PKQGVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120  
 61 IPKEQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120  
 Db 61 IPKEQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120  
 Qy 121 GAAGATSLCFYYPPLDFARTRLAADVGKSGTEREFGDCLVKTKSGDGLYQGFVS 180  
 121 GAAGATSLCFYYPPLDFARTRLAADVGKSGTEREFGDCLVKTKSGDGLYQGFVS 180  
 Db 121 GAAGATSLCFYYPPLDFARTRLAADVGKSGTEREFGDCLVKTKSGDGLYQGFVS 180  
 Qy 181 VQGIITRAAYFGYDTAKGMLPDKNTHIVSMIAQTVTAAGVSYPPDYRRRMM 240  
 181 VQGIITRAAYFGYDTAKGMLPDKNTHIVSMIAQTVTAAGVSYPPDYRRRMM 240  
 Db 181 VQGIITRAAYFGYDTAKGMLPDKNTHIVSMIAQTVTAAGVSYPPDYRRRMM 240  
 Qy 241 QSGRGADIMYTGIVDCWKIFRDEGKAFPGKAMSVNLKMGAFVLVLYDELK 296  
 241 QSGRGADIMYTGIVDCWKIFRDEGKAFPGKAMSVNLKMGAFVLVLYDELK 296  
 Db 241 QSGRGADIMYTGIVDCWKIFRDEGKAFPGKAMSVNLKMGAFVLVLYDELK 296

RESULT 5

US-09-810-644-32  
 ; Sequence 32, Application US/09810644  
 ; Patent No. US20020012992A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Anderson, Christen M.  
 ; APPLICANT: Davis, Robert E.  
 ; APPLICANT: Clevenger, William  
 ; APPLICANT: Wiley, Sandra Eileen  
 ; APPLICANT: Miller, Scott W.  
 ; APPLICANT: Szabo, Tomas R.  
 ; APPLICANT: Ghosh, Soumitra S.  
 ; APPLICANT: Moos, Walter H.  
 ; APPLICANT: Pei, Yanzhong  
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),  
 ; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
 ; FILE REFERENCE: 660088.420D3  
 ; CURRENT APPLICATION NUMBER: US/09/810.644  
 ; CURRENT FILING DATE: 2001-03-14  
 ; NUMBER OF SEQ ID NOS: 37  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 32  
 ; LENGTH: 298  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 ; US-09-810-644-32

Query Match 94.2%; Score 1454; DB 9; Length 298;  
 Best Local Similarity 92.6%; Pred. No. 3.5e-147;  
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Query 1 MTEOAIISFADPLAGIAAIAISKTAVAPIERVKLLLOVQHASKOITADKOKYKGIIDCVR 60  
 1 MTDALISFADPLAGIAAIAISKTAVAPIERVKLLLOVQHASKOITADKOKYKGIIDCVR 60  
 Db 1 MTDALISFADPLAGIAAIAISKTAVAPIERVKLLLOVQHASKOITADKOKYKGIIDCVR 60  
 Qy 1 PKQGVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120  
 61 IPKEQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120  
 Db 61 IPKEQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120  
 Qy 121 GAAGATSLCFYYPPLDFARTRLAADVGKSGTEREFGDCLVKTKSGDGLYQGFVS 180  
 121 GAAGATSLCFYYPPLDFARTRLAADVGKSGTEREFGDCLVKTKSGDGLYQGFVS 180  
 Db 121 GAAGATSLCFYYPPLDFARTRLAADVGKSGTEREFGDCLVKTKSGDGLYQGFVS 180  
 Qy 181 VQGIITRAAYFGYDTAKGMLPDKNTHIVSMIAQTVTAAGVSYPPDYRRRMM 240  
 181 VQGIITRAAYFGYDTAKGMLPDKNTHIVSMIAQTVTAAGVSYPPDYRRRMM 240  
 Db 181 VQGIITRAAYFGYDTAKGMLPDKNTHIVSMIAQTVTAAGVSYPPDYRRRMM 240  
 Qy 241 QSGRGADIMYTGIVDCWKIFRDEGKAFPGKAMSVNLKMGAFVLVLYDELK 296  
 241 QSGRGADIMYTGIVDCWKIFRDEGKAFPGKAMSVNLKMGAFVLVLYDELK 296  
 Db 241 QSGRGADIMYTGIVDCWKIFRDEGKAFPGKAMSVNLKMGAFVLVLYDELK 296

RESULT 6

US-09-185-904A-32  
 ; Sequence 32, Application US/09185904A  
 ; Patent No. US20020177185A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Anderson, Christen M.  
 ; APPLICANT: Davis, Robert E.  
 ; APPLICANT: Clevenger, William  
 ; APPLICANT: Wiley, Sandra Eileen  
 ; APPLICANT: Miller, Scott W.  
 ; APPLICANT: Szabo, Tomas R.  
 ; APPLICANT: Ghosh, Soumitra S.  
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE  
 ; TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS  
 ; TITLE OF INVENTION: THEREFOR  
 ; FILE REFERENCE: 660088.420  
 ; CURRENT APPLICATION NUMBER: US/09/185.904A  
 ; CURRENT FILING DATE: 1998-11-03  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 32  
 ; LENGTH: 298  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 ; US-09-185-904A-32

Query Match 94.2%; Score 1454; DB 10; Length 298;  
 Best Local Similarity 92.6%; Pred. No. 3.5e-147;  
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Query 1 MTEOAIISFADPLAGIAAIAISKTAVAPIERVKLLLOVQHASKOITADKOKYKGIIDCVR 60  
 1 MTDALISFADPLAGIAAIAISKTAVAPIERVKLLLOVQHASKOITADKOKYKGIIDCVR 60  
 Db 1 MTDALISFADPLAGIAAIAISKTAVAPIERVKLLLOVQHASKOITADKOKYKGIIDCVR 60  
 Qy 1 PKQGVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120  
 61 IPKEQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120  
 Db 61 IPKEQEVLSFWRGNLANVIRYPTQALNPAFKDKYKQIFLGVDKHTQFMRYFAGNLASG 120  
 Qy 121 GAAGATSLCFYYPPLDFARTRLAADVGKSGTEREFGDCLVKTKSGDGLYQGFVS 180  
 121 GAAGATSLCFYYPPLDFARTRLAADVGKSGTEREFGDCLVKTKSGDGLYQGFVS 180  
 Db 121 GAAGATSLCFYYPPLDFARTRLAADVGKSGTEREFGDCLVKTKSGDGLYQGFVS 180  
 Qy 181 VQGIITRAAYFGYDTAKGMLPDKNTHIVSMIAQTVTAAGVSYPPDYRRRMM 240  
 181 VQGIITRAAYFGYDTAKGMLPDKNTHIVSMIAQTVTAAGVSYPPDYRRRMM 240  
 Db 181 VQGIITRAAYFGYDTAKGMLPDKNTHIVSMIAQTVTAAGVSYPPDYRRRMM 240  
 Qy 241 QSGRGADIMYTGIVDCWKIFRDEGKAFPGKAMSVNLKMGAFVLVLYDELK 296  
 241 QSGRGADIMYTGIVDCWKIFRDEGKAFPGKAMSVNLKMGAFVLVLYDELK 296  
 Db 241 QSGRGADIMYTGIVDCWKIFRDEGKAFPGKAMSVNLKMGAFVLVLYDELK 296

RESULT 7

US-09-811-094-31  
 ; Sequence 31, Application US/09811094  
 ; Patent No. US20010044144A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Anderson, Christen M.  
 ; APPLICANT: Davis, Robert E.  
 ; APPLICANT: Clevenger, William  
 ; APPLICANT: Wiley, Sandra Eileen  
 ; APPLICANT: Miller, Scott W.  
 ; APPLICANT: Szabo, Tomas R.  
 ; APPLICANT: Ghosh, Soumitra S.  
 ; APPLICANT: Moos, Walter H.  
 ; APPLICANT: Pei, Yanzhong  
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),  
 ; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
 ; FILE REFERENCE: 660088.420D4  
 ; CURRENT APPLICATION NUMBER: US/09/811.094  
 ; CURRENT FILING DATE: 2001-03-14  
 ; NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 31  
 LENGTH: 297  
 TYPE: PRT  
 ORGANISM: Homo sapien  
 US-09-811-094-31

Query Match 89.8%; Score 1385.5; DB 9; Length 297;  
 Best Local Similarity 87.2%; Pred. No. 7.5e-140;  
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEQALSFADFLAGGIAAISTKTAVAPIERVKLLLOVQHASKOIAADKQYKGIIVDCIVR 60  
 DB 1 MGDHAWFLDPLDLAGAATAAASKTAVAPIERVKLLLOVQHASKOISAEKQYKGIIVDCIVR 60  
 QY 61 IPKEQGLSFWRGKLANVIRFPPTQALNFAFKDKYKQIFLGVDVRHQQFWRYFAGNLASG 120  
 DB 61 IPKEQGLSFWRGKLANVIRFPPTQALNFAFKDKYKQIFLGVDVRHQQFWRYFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDFARTRLAADVKGSGTEREFGDGLCVKITSKDGIRGLYOGFSVS 180  
 DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-AQREHFGDGLCVKITSKDGIRGLYOGFSVS 179  
 QY 181 VGGIIRAAVFGVYDTAKGMLPDPKXTHIVSWMTAQVTAVAGVSYFPDTRRRMM 240  
 DB 180 VGGIIRAAVFGVYDTAKGMLPDPKXTHIVSWMTAQVTAVAGVSYFPDTRRRMM 239  
 QY 241 QSGRKADIMYTGTVDCWKRKIFDEGGAFFKAMSNVLRMGGAFLVLYDEIKKYV 298  
 DB 240 QSGRKADIMYTGTVDCWKRKIADEGAKAFKAMSNVLRMGGAFLVLYDEIKKYV 297

## RESULT 8

US-09-810-644-31  
 Sequence 31, Application US/09810644  
 Patent No. US20020012992A1  
 GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.  
 APPLICANT: Davis, Robert E.  
 APPLICANT: Clevenger, William  
 APPLICANT: Willey, Sandra Eileen  
 APPLICANT: Willey, Scott W.  
 APPLICANT: Szabo, Tomas R.  
 APPLICANT: Ghosh, Soumitra S.  
 APPLICANT: Moos, Walter H.  
 APPLICANT: Pei, Yanzhong  
 TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),  
 TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
 FILE REFERENCE: 660088.420D3  
 CURRENT APPLICATION NUMBER: US/09/810.644  
 CURRENT FILING DATE: 2001-03-14  
 NUMBER OF SEQ ID NOS: 37  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 31  
 LENGTH: 297  
 TYPE: PRT  
 ORGANISM: Homo sapien  
 US-09-810-644-31

Query Match 89.8%; Score 1385.5; DB 9; Length 297;  
 Best Local Similarity 87.2%; Pred. No. 7.5e-140;  
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEQALSFADFLAGGIAAISTKTAVAPIERVKLLLOVQHASKOIAADKQYKGIIVDCIVR 60  
 DB 1 MGDHAWFLDPLDLAGAATAAASKTAVAPIERVKLLLOVQHASKOISAEKQYKGIIVDCIVR 60  
 QY 61 IPKEQGLSFWRGKLANVIRFPPTQALNFAFKDKYKQIFLGVDVRHQQFWRYFAGNLASG 120  
 DB 61 IPKEQGLSFWRGKLANVIRFPPTQALNFAFKDKYKQIFLGVDVRHQQFWRYFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDFARTRLAADVKGSGTEREFGDGLCVKITSKDGIRGLYOGFSVS 180  
 DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-AQREHFGDGLCVKITSKDGIRGLYOGFSVS 179

DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-AQREHFGDGLCVKITSKDGIRGLYOGFSVS 179  
 QY 181 VGGIIRAAVFGVYDTAKGMLPDPKXTHIVSWMTAQVTAVAGVSYFPDTRRRMM 240  
 DB 180 VGGIIRAAVFGVYDTAKGMLPDPKXTHIVSWMTAQVTAVAGVSYFPDTRRRMM 239  
 QY 241 QSGRKADIMYTGTVDCWKRKIFDEGGAFFKAMSNVLRMGGAFLVLYDEIKKYV 298  
 DB 240 QSGRKADIMYTGTVDCWKRKIADEGAKAFKAMSNVLRMGGAFLVLYDEIKKYV 297

## RESULT 9

US-09-185-904A-31  
 Sequence 31, Application US/09185904A  
 Patent No. US20020177185A1  
 GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.  
 APPLICANT: Davis, Robert E.  
 APPLICANT: Clevenger, William  
 APPLICANT: Willey, Sandra Eileen  
 APPLICANT: Willey, Scott W.  
 APPLICANT: Szabo, Tomas R.  
 APPLICANT: Ghosh, Soumitra S.  
 TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE  
 TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS  
 TITLE OF INVENTION: THEREFOR  
 FILE REFERENCE: 660088.420  
 CURRENT APPLICATION NUMBER: US/09/185.904A  
 CURRENT FILING DATE: 1998-11-03  
 NUMBER OF SEQ ID NOS: 33  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 31  
 LENGTH: 297  
 TYPE: PRT  
 ORGANISM: Homo sapien  
 US-09-185-904A-31

Query Match 89.8%; Score 1385.5; DB 10; Length 297;  
 Best Local Similarity 87.2%; Pred. No. 7.5e-140;  
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEQALSFADFLAGGIAAISTKTAVAPIERVKLLLOVQHASKOIAADKQYKGIIVDCIVR 60  
 DB 1 MGDHAWFLDPLDLAGAATAAASKTAVAPIERVKLLLOVQHASKOISAEKQYKGIIVDCIVR 60  
 QY 61 IPKEQGLSFWRGKLANVIRFPPTQALNFAFKDKYKQIFLGVDVRHQQFWRYFAGNLASG 120  
 DB 61 IPKEQGLSFWRGKLANVIRFPPTQALNFAFKDKYKQIFLGVDVRHQQFWRYFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDFARTRLAADVKGSGTEREFGDGLCVKITSKDGIRGLYOGFSVS 180  
 DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-AQREHFGDGLCVKITSKDGIRGLYOGFSVS 179  
 QY 181 VGGIIRAAVFGVYDTAKGMLPDPKXTHIVSWMTAQVTAVAGVSYFPDTRRRMM 240  
 DB 180 VGGIIRAAVFGVYDTAKGMLPDPKXTHIVSWMTAQVTAVAGVSYFPDTRRRMM 239  
 QY 241 QSGRKADIMYTGTVDCWKRKIFDEGGAFFKAMSNVLRMGGAFLVLYDEIKKYV 298  
 DB 240 QSGRKADIMYTGTVDCWKRKIADEGAKAFKAMSNVLRMGGAFLVLYDEIKKYV 297

## RESULT 10

US-10-029-386-32501  
 Sequence 32501, Application US/10029386  
 Publication No. US20030194704A1  
 GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.  
 APPLICANT: Rank, David R.  
 APPLICANT: Hanzel, David K.  
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI  
 FILE REFERENCE: AEOMICA-X-2

```

; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32501
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004000.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.95
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96
; OTHER INFORMATION: SWISSPROT HIT: P05141, EVALU 2.00e-83
; US-10-029-386-32501

Query Match          52.6%; Score 811; DB 12; Length 179;
Best Local Similarity 93.3%; Pred. No. 1.2e-78;
Matches 152; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Oy 38 VOHASKQIADKQYGIYDCTVIRIKRQGVLSFMRGNLANVIRYPTQALNPAFDKXKQ 97
    |||||
Db 1 VOHASKQITADQYGIIDCVIRIKRQGVLSFMRGNLANVIRYPTQALNPAFDKXKQ 60
    |||||

Oy 98 IFLGVDKHTQFMRFYFAGNLASGAAGATSLCFVYPLDFARTLADYKSGTEREPFGL 157
    |||||
Db 61 IFLGVDKHTQFMRFYFAGNLASGAAGATSLCFVYPLDFARTLADYKSGTEREPFGL 120
    |||||

Oy 158 GDCLVKITKSDGIRGLYOGFSVSVGGIITRYAAYFGVYDTAKG 200
    |||||
Db 121 GDCLVKITKSDGIRGLYOGFSVSVGGIITRYAAYFGVYDTAKG 163
    |||||

RESULT 11
; US-10-032-585-7194
; Sequence 7194, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jlang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7194
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Candida albicans
; US-10-032-585-7194

Query Match          51.1%; Score 788.5; DB 12; Length 301;
Best Local Similarity 54.7%; Pred. No. 6.3e-76;
Matches 162; Conservative 42; Mismatches 83; Indels 9; Gaps 5;

Oy 7 SPANDFLAGIAAIAISKTAVAPIERVKLLQVQ-HASKQIADKQYGIYDCTVIRIPKQ 65
    |||||
Db 5 NFQVDFMVGVAASAKTAAPIERVKLLIQNODSMIKQSLERKRYTIVOCFRTADE 64
    |||||

Oy 66 GVLSEMRGNLANVIRYPTQALNPAFKQIKQIFLGVDKHTQFMRFYFAGNLASGAAGA 125
    |||||
Db 65 GVLSEMRGNLANVIRYPTQALNPAFKQIKQIFLGVDKHTQFMRFYFAGNLASGAAGA 122
    |||||

Oy 126 TSLCFVYPLDFARTLADY--GKSGTEREPFGLGDCLVKITKSDGIRGLYOGFSVSVG 183
    |||||
Db 123 TSLAFVYPLDFARTLADYSSKSDGKREFNGLVDVYKKTILASDGLIGLFGSPSYIG 182
    |||||

Oy 184 IIRYAAAYFGVYDTAKG-MLPDPKNTHTIVSWMLAQTVTAAGVSVYPTVRRRMQOS 242
    |||||
```

```

; DB 183 IIVYRGLYFGLYDSLKPVVLVGPLEGSLASFLLGMAVTTGASTASVYPLDTRRRMMQTS 242
    |||||
Oy 243 GRKADIMYGTGVCQWKRIFRDEGGKAFPKKAMSIVLRGMGAPVLYYDLSKKYI 298
    |||||
Db 243 GQA--VKYDGAIDCFKRKVAAGVSLFKCGGANILRGVAGAGVSLYDLOQLVIL 295
    |||||

RESULT 12
; US-09-801-368-252
; Sequence 252, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 252
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-09-801-368-252

Query Match          49.3%; Score 760.5; DB 10; Length 318;
Best Local Similarity 53.7%; Pred. No. 6.8e-73;
Matches 159; Conservative 42; Mismatches 86; Indels 9; Gaps 5;

Oy 7 SPANDFLAGIAAIAISKTAVAPIERVKLLQVQ-HASKQIADKQYGIYDCTVIRIPKQ 65
    |||||
Db 22 NFLIDFLMGVSAVAAKTAAPIERVKLLIQNODSMIKQSLDRKVGILDCFRRTAOE 81
    |||||

Oy 66 GVLSEMRGNLANVIRYPTQALNPAFKQIKQIFLGVDKHTQFMRFYFAGNLASGAAGA 125
    |||||
Db 82 GVLSEMRGNLANVIRYPTQALNPAFKQIKQIFLGVDKHTQFMRFYFAGNLASGAAGA 139
    |||||

Oy 126 TSLCFVYPLDFARTLAD--VGKSGTEREPFGLGDCLVKITKSDGIRGLYOGFSVSVG 183
    |||||
Db 140 LSLFVYSLDYARKRLAADSSSKGARGQPNGLIDYKKTILASDGLYKGLPSYVG 199
    |||||

Oy 184 IIRYAAAYFGVYDTAKG-MLPDPKNTHTIVSWMLAQTVTAAGVSVYPTVRRRMQOS 242
    |||||
Db 200 IIVYRGLYFGLYDSLKPVVLVGPLEGSLASFLLGMAVTTGASTASVYPLDTRRRMMQTS 259
    |||||

Oy 243 GRKADIMYGTGVCQWKRIFRDEGGKAFPKKAMSIVLRGMGAPVLYYDLSKKYI 298
    |||||
Db 260 GQA--VKYDGAIDCFKRKVAAGVSLFKCGGANILRGVAGAGVSLYDLOQLVIL 312
    |||||

RESULT 13
; US-09-734-569-170
; Sequence 170, Application US/09734569
; Patent No. US20020064816A1
; GENERAL INFORMATION:
; APPLICANT: Lerchl, Jens
```

Query Match	48.6%	Score 749.5	DB 9	Length 386
Best Local Similarity	53.4%	Pred No. 1.3e-71		
Matches 157	Conservative 44	Mismatches 84	Indels 9	Gaps 5

RESULT 14  
US-10-128-714-3338

```

: PRIOR FILING DATE: 2001-07-09
: PRIOR APPLICATION NUMBER: US 60/316,362
: PRIOR FILING DATE: 2001-08-31
: NUMBER OF SEQ ID NOS: 8603
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 3338
: LENGTH: 308
: TYPE: PR1
: ORGANISM: Aspergillus fumigatus
: US-10-128-714-3338

```

Query Match	47.8%;	Score 737;	DB 15;	Length 308;
Best Local Similarity	51.7%;	Pred. No. 2.1e-70;		
Matches 154;	Conservative 47;	Mismatches 85;	Indels 12;	Gaps 6;

QY		7	SFADPFLAGGIAAIIKSTVAPIERVKLLLOVHASKOIAA---DKYKGIVDCIVRLEPK	63
Db		7	AFTDSFAVGVSAAVSKTAAPIRIKTL--VNQODEMIRAGRDRKKNGLIDCFERRAQ	64
QY		64	EQVLGSFWRGNLAVNIFFPTQALNFAFKDXYKQIFLGGVDKHTQPMWRYPAGNTLASGGA	123
Db		65	AEGWMSLMRGTAANVIIFYPTQALNFPRDYKKMFAYKKDR-DGYAKMMNGNLASGGA	123
QY		124	GATSLCVCVPFLDFARTRLADV--GKSGTEEPFRGLDGCIVKIKRSGIRGLYGGSFSV	181
Db		124	GATSLLEVVISLDYKRTRLANDAKSAKGGGEHQFGLLDYRKTLASDSIAGLYKGFSGSV	183
QY		182	OQIIITYBAAYFGVYDIKAG-MLPDPKNTHLVSMMLAQVTYTAGVGVSYPEDTVRRRMM	240
Db		184	LGIIVYGLTFEGMWDSFKPVVLVSLSEGSFLASFILGMTVTTGTAGIASYPEDTIRRMM	243
QY		241	QSGRKADIMWTGVDCKRTFRDEGKAAPFKKAMSNVLGMGGAFTVLVYLDELKYI	298
Db		244	TSGA---VYKKSLSDAKQILAKEGVKSLFKKGANILLGVAAAGVSIYDVQVLL	298

**RESULT 15**

US-10-128-714-8338  
; Sequence 8338, Application US/10128714  
; Publication No. US20030119013A1

```

? GENERAL INFORMATION:
? APPLICANT: Jiang, Bo
? APPLICANT: Hu, Wengdi
? APPLICANT: Tishkoff, Daniel
? APPLICANT: Zamudio, Carlos
? APPLICANT: Eroshkin, Alexey M
? APPLICANT: Lemieux, Sebastien M
? TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
? TITLE OF INVENTION: Methods of Use
? FILE REFERENCE: 10182-018-999
? CURRENT APPLICATION NUMBER: US/10/128,714
? CURRENT FILING DATE: 2002-04-23
? PRIOR APPLICATION NUMBER: US 60/285,697
? PRIOR FILING DATE: 2001-04-23
? PRIOR APPLICATION NUMBER: US 60/287,066
? PRIOR FILING DATE: 2001-04-27
? PRIOR APPLICATION NUMBER: US 60/295,890
? PRIOR FILING DATE: 2001-06-05
? PRIOR APPLICATION NUMBER: US 60/303,899
? PRIOR FILING DATE: 2001-07-09
? PRIOR APPLICATION NUMBER: US 60/316,362
? PRIOR FILING DATE: 2001-08-31
? NUMBER OF SEQ ID NOS: 8603
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 8338
? LENGTH: 308
? TYPE: PRT
? ORGANISM: Aspergillus fumigatus
? US-10-128-714-8338

```

Query Match	47.8%;	Score 737;	DB 15;	Length 308;
Best Local Similarity	51.7%;	Pred. No. 2.1e-70;		
Matches 154;	Conservative 47;	Mismatches 85;	Indels 12;	Gaps 6;



**THIS PAGE BLANK (USPTO)**

QY	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
QY	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Db	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
QY	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Db	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
QY	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	8																				

```

RESULT 2
US-09-434-354-48
; Sequence 48, Application US/09434354
; Patent No. 6562563
; GENERAL INFORMATION:
; APPLICANT: Murphy, Anne N.
; APPLICANT: Cleverger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Andreyev, Alexander Y.
; APPLICANT: Frigert, Luciano G.
; APPLICANT: Velicelbel, Gonul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
; TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
; FILE REFERENCE: 660088.433
; CURRENT APPLICATION NUMBER: US/09/434,354
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-434-354-48

Query Match          94.2%; Score 1454; DB 4; Length 298;
Best Local Similarity 92.6%; Pred. No. 5.2e-15;
Matches 274; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEQALSPADFLAGIAGIAAISTAVAPIERVKLLQVQHASQIADKQYKGIIVDCIVR 60
DB 1 MTDALSPADFLAGIAGIAAISTAVAPIERVKLLQVQHASQIADKQYKGIIVDCIVR 60
QY 61 IPKEQGLSWFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLASG 120
DB 61 IPKEQGLSWFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLADVKGSGTEREFGDCLVYITKSDGIRGLYQGRSVS 180
DB 121 GAAGATSLCFVYPLDFARTLADVKGSGTEREFGDCLVYITKSDGIRGLYQGRSVS 180
QY 181 VQGIIRYRAAFVGYVDTAKGMLPDPKNTIYVSMIAQTYTAVAGVSYFPDTRRRMM 240
DB 181 VQGIIRYRAAFVGYVDTAKGMLPDPKNTIYVSMIAQTYTAVAGVSYFPDTRRRMM 240
QY 241 QSGRKGADIMYTGTCWKRKIFRDEGKAFKFGAMSVNLRGMGAPVLYVDELKX 296
DB 241 QSGRKGADIMYTGTCWKRKIFRDEGKAFKFGAMSVNLRGMGAPVLYVDELKX 296

RESULT 3
US-08-961-871-10
; Sequence 10, Application US/08961871
; Patent No. 6013858
; GENERAL INFORMATION:
; APPLICANT: Wallace, Douglas C.
; APPLICANT: Graham, Brett H.
; APPLICANT: Macgregor, Grant R.
; TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
; TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,871
; FILING DATE: 31-Oct-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/030,017
; FILING DATE: 01-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 78-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-961-871-10

Query Match          91.5%; Score 1412; DB 3; Length 298;
Best Local Similarity 88.6%; Pred. No. 2.9e-15;
Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEQALSPADFLAGIAGIAAISTAVAPIERVKLLQVQHASQIADKQYKGIIVDCIVR 60
DB 1 MTDALSPADFLAGIAGIAAISTAVAPIERVKLLQVQHASQIADKQYKGIIVDCIVR 60
QY 61 IPKEQGLSWFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLASG 120
DB 61 IPKEQGLSWFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLADVKGSGTEREFGDCLVYITKSDGIRGLYQGRSVS 180
DB 121 GAAGATSLCFVYPLDFARTLADVKGSGTEREFGDCLVYITKSDGIRGLYQGRSVS 180
QY 181 VQGIIRYRAAFVGYVDTAKGMLPDPKNTIYVSMIAQTYTAVAGVSYFPDTRRRMM 240
DB 181 VQGIIRYRAAFVGYVDTAKGMLPDPKNTIYVSMIAQTYTAVAGVSYFPDTRRRMM 240
QY 241 QSGRKGADIMYTGTCWKRKIFRDEGKAFKFGAMSVNLRGMGAPVLYVDELKX 298
DB 241 QSGRKGADIMYTGTCWKRKIFRDEGKAFKFGAMSVNLRGMGAPVLYVDELKX 298

RESULT 4
US-09-434-354-47
; Sequence 47, Application US/09434354
; Patent No. 6562563
; GENERAL INFORMATION:
; APPLICANT: Murphy, Anne N.
; APPLICANT: Cleverger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Andreyev, Alexander Y.
; APPLICANT: Frigert, Luciano G.
; APPLICANT: Velicelbel, Gonul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
; TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
; FILE REFERENCE: 660088.433
; CURRENT APPLICATION NUMBER: US/09/434,354
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 47
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapien

```



US-09-434-354-47

Query Match 89.8%; Score 1385.5; DB 4; Length 297;  
 Best Local Similarity 87.2%; Pred No. 2,9e-148;  
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEQASIPAKDFLAGIAAISKTAIVAPIERVKLLQVQHASKQIADKQYKGIIVDCIVR 60  
 Db 1 MGDHMSFLKDFLAGVAVAASKTAVAPIERVKLLQVQHASKQIADKQYKGIIVDCIVR 60  
 QY 61 IPKQGVLSFWRKGNLANIRFPPTALNPAFKQDKTKQIFLGVDVGHQTPWRYFAGNLASG 120  
 Db 61 IPKQGVLSFWRKGNLANIRFPPTALNPAFKQDKTKQIFLGVDVGHQTPWRYFAGNLASG 120  
 QY 121 GAAGATSLCFYYPDFARTPLAADVYKSGTEREFGLDGLCKIKRSGDGLYOGFVS 180  
 Db 121 GAAGATSLCFYYPDFARTPLAADVYKSGTEREFGLDGLCKIKRSGDGLYOGFVS 179  
 QY 181 VGGIIYRAAYFGVYDTAKGMLPDRKNTHTIVSMIAQTVAVAGVSVYPTVRRMM 240  
 Db 180 VGGIIYRAAYFGVYDTAKGMLPDRKNTHTIVSMIAQTVAVAGVSVYPTVRRMM 239  
 QY 241 OSRGKALIMTGTIDCRKIFRDEGKAFKFGKANSNLRGKGFVLYVDELKKVI 238  
 Db 240 OSRGKALIMTGTIDCRKIFRDEGKAFKFGKANSNLRGKGFVLYVDELKKVI 237

RESULT 5  
 US-09-996-243-289

/ Sequence 289, Application US/09996243

/ Patent No. 6478825

/ GENERAL INFORMATION:

/ APPLICANT: Ashkenazi, Avi J.

/ APPLICANT: Baker, Kevin P.

/ APPLICANT: Bostein, David

/ APPLICANT: Desnoyers, Luc

/ APPLICANT: Eaton, Dan L.

/ APPLICANT: Ferrara, Napoleone

/ APPLICANT: Fong, Sherman

/ APPLICANT: Gerber, Hanspeter

/ APPLICANT: Gerritsen, Mary E.

/ APPLICANT: Goddard, Audrey

/ APPLICANT: Godowski, Paul J.

/ APPLICANT: Grimaldi, J. Christopher

/ APPLICANT: Gurney, Austin L.

/ APPLICANT: Kljavin, Ivar J.

/ APPLICANT: Napier, Mary A.

/ APPLICANT: Pan, James

/ APPLICANT: Paoni, Nicholas F.

/ APPLICANT: Roy, Margaret Ann

/ APPLICANT: Stewart, Timothy A.

/ APPLICANT: Tunas, Daniel

/ APPLICANT: Watanabe, Colin K.

/ APPLICANT: Williams, P. Mickey

/ APPLICANT: Wood, William I.

/ APPLICANT: Zhang, Zemin

/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

/ TITLE OF INVENTION: Acids Encoding the Same

/ FILE REFERENCE: P2730PC13

/ CURRENT APPLICATION NUMBER: US/09/996,243

/ PRIOR FILING DATE: 2001-11-14

/ PRIOR APPLICATION NUMBER: 60/049787

/ PRIOR FILING DATE: 1997-06-16

/ PRIOR APPLICATION NUMBER: 60/062250

/ PRIOR FILING DATE: 1997-10-17

/ PRIOR APPLICATION NUMBER: 60/065186

/ PRIOR FILING DATE: 1997-11-12

/ PRIOR APPLICATION NUMBER: 60/065311

/ PRIOR FILING DATE: 1997-11-13

/ PRIOR APPLICATION NUMBER: 60/066770

/ PRIOR FILING DATE: 1997-11-24

/ PRIOR APPLICATION NUMBER: 60/075945

/ PRIOR FILING DATE: 1998-02-25

/ PRIOR APPLICATION NUMBER: 60/089598

/ PRIOR APPLICATION NUMBER: 60/078910  
 / PRIOR FILING DATE: 1998-03-20  
 / PRIOR APPLICATION NUMBER: 60/083322  
 / PRIOR FILING DATE: 1998-04-28  
 / PRIOR APPLICATION NUMBER: 60/084600  
 / PRIOR FILING DATE: 1998-05-07  
 / PRIOR APPLICATION NUMBER: 60/087106  
 / PRIOR FILING DATE: 1998-05-28  
 / PRIOR APPLICATION NUMBER: 60/087607  
 / PRIOR FILING DATE: 1998-06-02  
 / PRIOR APPLICATION NUMBER: 60/087609  
 / PRIOR FILING DATE: 1998-06-02  
 / PRIOR APPLICATION NUMBER: 60/087759  
 / PRIOR FILING DATE: 1998-06-02  
 / PRIOR APPLICATION NUMBER: 60/087827  
 / PRIOR FILING DATE: 1998-06-03  
 / PRIOR APPLICATION NUMBER: 60/088021  
 / PRIOR FILING DATE: 1998-06-04  
 / PRIOR APPLICATION NUMBER: 60/088025  
 / PRIOR FILING DATE: 1998-06-04  
 / PRIOR APPLICATION NUMBER: 60/088026  
 / PRIOR FILING DATE: 1998-06-04  
 / PRIOR APPLICATION NUMBER: 60/088028  
 / PRIOR FILING DATE: 1998-06-04  
 / PRIOR APPLICATION NUMBER: 60/088029  
 / PRIOR FILING DATE: 1998-06-04  
 / PRIOR APPLICATION NUMBER: 60/088030  
 / PRIOR FILING DATE: 1998-06-04  
 / PRIOR APPLICATION NUMBER: 60/088033  
 / PRIOR FILING DATE: 1998-06-04  
 / PRIOR APPLICATION NUMBER: 60/088326  
 / PRIOR FILING DATE: 1998-06-04  
 / PRIOR APPLICATION NUMBER: 60/088167  
 / PRIOR FILING DATE: 1998-06-05  
 / PRIOR APPLICATION NUMBER: 60/088202  
 / PRIOR FILING DATE: 1998-06-05  
 / PRIOR APPLICATION NUMBER: 60/088212  
 / PRIOR FILING DATE: 1998-06-05  
 / PRIOR APPLICATION NUMBER: 60/088217  
 / PRIOR FILING DATE: 1998-06-05  
 / PRIOR APPLICATION NUMBER: 60/088655  
 / PRIOR FILING DATE: 1998-06-09  
 / PRIOR APPLICATION NUMBER: 60/088734  
 / PRIOR FILING DATE: 1998-06-10  
 / PRIOR APPLICATION NUMBER: 60/088738  
 / PRIOR FILING DATE: 1998-06-10  
 / PRIOR APPLICATION NUMBER: 60/088742  
 / PRIOR FILING DATE: 1998-06-10  
 / PRIOR APPLICATION NUMBER: 60/088810  
 / PRIOR FILING DATE: 1998-06-10  
 / PRIOR APPLICATION NUMBER: 60/088824  
 / PRIOR FILING DATE: 1998-06-10  
 / PRIOR APPLICATION NUMBER: 60/088826  
 / PRIOR FILING DATE: 1998-06-10  
 / PRIOR APPLICATION NUMBER: 60/088858  
 / PRIOR FILING DATE: 1998-06-11  
 / PRIOR APPLICATION NUMBER: 60/088861  
 / PRIOR FILING DATE: 1998-06-11  
 / PRIOR APPLICATION NUMBER: 60/088876  
 / PRIOR FILING DATE: 1998-06-11  
 / PRIOR APPLICATION NUMBER: 60/089105  
 / PRIOR FILING DATE: 1998-06-12  
 / PRIOR APPLICATION NUMBER: 60/089440  
 / PRIOR FILING DATE: 1998-06-16  
 / PRIOR APPLICATION NUMBER: 60/089512  
 / PRIOR FILING DATE: 1998-06-16  
 / PRIOR APPLICATION NUMBER: 60/089514  
 / PRIOR FILING DATE: 1998-06-16  
 / PRIOR APPLICATION NUMBER: 60/089532  
 / PRIOR FILING DATE: 1998-06-17  
 / PRIOR APPLICATION NUMBER: 60/089538  
 / PRIOR FILING DATE: 1998-06-17  
 / PRIOR APPLICATION NUMBER: 60/089598

PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089595
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089600
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089655
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089800
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/089900
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/089944
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/089946
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/089955
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/090025
PRIOR FILING DATE:	1998-06-22
PRIOR APPLICATION NUMBER:	60/090252
PRIOR FILING DATE:	1998-06-22
PRIOR APPLICATION NUMBER:	60/090255
PRIOR FILING DATE:	1998-06-22
PRIOR APPLICATION NUMBER:	60/090344
PRIOR FILING DATE:	1998-06-23
PRIOR APPLICATION NUMBER:	60/090355
PRIOR FILING DATE:	1998-06-23
PRIOR APPLICATION NUMBER:	60/090435
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090444
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090445
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090472
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090533
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090540
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090544
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090555
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090676
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090678
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090696
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090699
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090699
PRIOR FILING DATE:	1998-06-26
PRIOR APPLICATION NUMBER:	60/090866
PRIOR FILING DATE:	1998-06-26
PRIOR APPLICATION NUMBER:	60/091366
PRIOR FILING DATE:	1998-07-01
PRIOR APPLICATION NUMBER:	60/091478
PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/091544
PRIOR FILING DATE:	1998-07-01
PRIOR APPLICATION NUMBER:	60/091519
PRIOR FILING DATE:	1998-07-02

PRIOR APPLICATION NUMBER: 60/091626  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091633  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

[illegible]

	Query Match	20.2%	Score 311,	DB 3,	Length 469;	
	Best Local Similarity	29.4%;	Pred. No. 1.7e-26;			
	Matches	88;	Conservative	62;	Mismatches 111;	Indels 38; Gaps 11;
QY	10	KDLFAGTAAIAISTANVAPIERVVLLIQVHASKQIADKRYKVGDCTIVAPKEQGVLG	69			
	:	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :
Db	188	RHHVAGGGAGAVERSTCAPLDRLKVLNQV--HASR-----SNMNCIVGGFTQMIREGSAKS	241			
QY	70	FWRGNLANVIRYPTQLNLNFAFKDKYKQIFLGVDXKHQTQFWRYPAFGNLSAAGGAATSLC	129			
	:	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :
Db	242	LWNGNGINVLKIAPESAIKFMAYEQMR--LVGSDQET---LRHERLVAASGLGALIAQS	296			
QY	130	FVYPFLDPAFRTRLAADVGKSTEREFRLGDCLVKITKSDGI RGLYYQGSVSVOGIIIRA	189			
	:	: : : : :	: : : : :	: : : : :	: : : : :	: : : : :

Db 297 SIYMEVLTAKTMA--LRKTG---QYSGMLDCARLLIAKEGVAAFYKGIYPMNLGIIPYAG 351  
 Oy 190 AYFGYDTAKGMLPDPKATHI-----VVSMTIAQTVTAAG--VVSYPPTVRRR 237  
 Db 352 IDLAVETL-----KNTWLORYAVNSADPGVFLILACGIISSICGQIASIPILAVRTR 404  
 Oy 238 MMOSGRGADIMYGTVDGWRKIFRDEGKAFKFGAMSNTLRGAGAFV--LVLYDELK 295  
 Db 405 MOAQASIGAPEVMTSSL--FKQILRTGAGFGLYRGLAPNFMKVI PAVISISVYVENLK 461

# RESULT 7

US-09-312-283C-339  
 ; Sequence 339, Application US/09312283C  
 ; Patent No. 6573095  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Watson, James D.  
 ; APPLICANT: Strachan, Lorna  
 ; APPLICANT: Sleeman, Matthew  
 ; APPLICANT: Onrust, Rene  
 ; APPLICANT: Murison, James G.  
 ; APPLICANT: Kumble, Krishanand D.  
 ; TITLE OF INVENTION: Compositions Isolated from Skin Cells  
 ; TITLE OF INVENTION: and Methods for Their Use  
 ; FILE REFERENCE: 11000.1011C2  
 ; CURRENT APPLICATION NUMBER: US/09/312,283C  
 ; CURRENT FILING DATE: 1999-05-14  
 ; NUMBER OF SEQ ID NOS: 425  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 339  
 ; LENGTH: 469  
 ; TYPE: PRT  
 ; ORGANISM: Mouse  
 ; US-09-312-283C-339

Query Match 20.2%; Score 311; DB 4; Length 469;  
 Best Local Similarity 29.4%; Pred. No. 1.7e-26;  
 Matches 88; Conservative 62; Mismatches 111; Indels 38; Gaps 11;

Oy 10 KDFLAGGIAAIAISTKAVAPIERVKLLIOVQHASKIADKQYKGVDCIVIRPEQVLS 69  
 Db 188 RHLVAGGAGAVSRTCTPLRLKVLMOV--HASR-----SNMCTVGGFTQIREGAKS 241  
 Oy 70 FMRGLAVIRVYFPFOALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLSGGAAGATSLC 129  
 Db 242 LMRNGINVLKIAPESAIKFYAYEQMK--LVGSDQET--LRHERLVAGSLAGALIAQS 296  
 Oy 130 FVYPLDFARTRLADVGKSGTEREFGDCLVITKSDGIRGLYOGFSVSVOGIIVYRA 189  
 Db 297 SIYMEVLTAKTMA--LRKTG---QYSGMLDCARLLIAKEGVAAFYKGIYPMNLGIIPYAG 351  
 Oy 190 AYFGYDTAKGMLPDPKATHI-----VVSMTIAQTVTAAG--VVSYPPTVRRR 237  
 Db 352 IDLAVETL-----KNTWLORYAVNSADPGVFLILACGIISSICGQIASIPILAVRTR 404  
 Oy 238 MMOSGRGADIMYGTVDGWRKIFRDEGKAFKFGAMSNTLRGAGAFV--LVLYDELK 295  
 Db 405 MOAQASIGAPEVMTSSL--FKQILRTGAGFGLYRGLAPNFMKVI PAVISISVYVENLK 461

# RESULT 8

US-09-482-273-118  
 ; Sequence 118, Application US/09482273  
 ; Patent No. 6534631  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: 71 Human Secreted Proteins  
 ; FILE REFERENCE: P2030P1  
 ; CURRENT APPLICATION NUMBER: US/09/482,273  
 ; EARLIER FILING DATE: 2000-01-13  
 ; EARLIER APPLICATION NUMBER: PCT/US99/15849  
 ; EARLIER FILING DATE: 1999-07-14  
 ; EARLIER APPLICATION NUMBER: 60/092,921

; EARLIER FILING DATE: 1998-07-15  
 ; EARLIER APPLICATION NUMBER: 60/092,922  
 ; EARLIER FILING DATE: 1998-07-15  
 ; EARLIER APPLICATION NUMBER: 60/092,956  
 ; EARLIER FILING DATE: 1998-07-15  
 ; NUMBER OF SEQ ID NOS: 267  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 118  
 ; LENGTH: 335  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (335)  
 ; OTHER INFORMATION: Xaa equals stop translation  
 ; US-09-482-273-118

Query Match 18.5%; Score 286; DB 4; Length 335;  
 Best Local Similarity 29.0%; Pred. No. 6.9e-24;  
 Matches 87; Conservative 50; Mismatches 133; Indels 30; Gaps 8;

Oy 10 KDFLAGGIAAIAISTKAVAPIERVKLLIOVQHAS-----KQIADKQYKGVDCIVIRPE 64  
 Db 51 KPFYGGGLASIVAEFGTFPVDLTETRLQVQGSIDARFKEI---KYRGMFHALFRICKE 106  
 Oy 65 QGVLSFMRGLAVIRVYFPFOALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLSGGAAG 124  
 Db 107 EGVLAISGIAIPALLRQASGTIKIGIYQSLKRLFVRLEDET-----LILNMCGVSVG 161  
 Oy 125 ATSLCFVYPLDFARTRLADVGKSGTEREFGDCLVITKSDGIRGLYOGFSVSVOGI 184  
 Db 162 VISSTIANPDTVLKIRNQA---QGSIFQSGMIGS-FIDLYQDEGFTGLMRGVVPTAORA 216  
 Oy 185 ILYAAIFGYVDTK-----GMLPDPKATHIYVSMIAQTVTAAGVVSYPPTVRRR 238  
 Db 217 AIVGVVELPYVDITKRLILSGMMDITLIFVSSF-----TCGLAGALASNPVDVVRTRM 272  
 Oy 239 MMOSGRGADIMYGTVDGWRKIFRDEGKAFKFGAMSNTLR--GMGAPVLVLYDELK 297  
 Db 273 MNCRAIVGHVDLYKGTVDGILKMKHGEFPALYKGFPMNLRLGSPNNIIFPIYEQRLRL 332

# RESULT 9

US-09-501-558-2  
 ; Sequence 2, Application US/09501558  
 ; Patent No. 6403784  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; APPLICANT: Mathur, Brian  
 ; APPLICANT: Zambrowicz, Brian  
 ; APPLICANT: Sande, Arthur T.  
 ; TITLE OF INVENTION: No. 6403784e1 Human Uncoupling Proteins and  
 ; FILE REFERENCE: LEX-0012-USA  
 ; CURRENT APPLICATION NUMBER: US/09/501,558  
 ; CURRENT FILING DATE: 2000-02-09  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 291  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-501-558-2

Query Match 18.4%; Score 283.5; DB 4; Length 291;  
 Best Local Similarity 28.9%; Pred. No. 1.1e-23;  
 Matches 87; Conservative 54; Mismatches 129; Indels 31; Gaps 9;

Oy 10 KDFLAGGIAAIAISTKAVAPIERVKLLIOVQHAS-----KQIADKQYKGVDCIVIRPE 64  
 Db 7 KPFYGGGLASITABCGTFPIDLTETRLQILOGTNDAKFKEI---RYRGLHALVIRIGRE 62  
 Oy 65 QGVLSFMRGLAVIRVYFPFOALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLSGGAAG 124

```
Db      63 EGKALVSGIAPAMLRQASVGTIKIGTYQSLKRLFIREDDET-----LPIINVIGILSG 117
Qy      125 ATSLCFYPLDPFARTRLAADVGKSGTEREFRGLDCLVKTIKSGTIGLVQGSFVSQGI 184
Db      118 VIISTIANPFDVKIRMOA---QSENTIQ--GGMIGNFMNIYQOGTGLMWGVSLEYTAQRA 172
Qy      185 IIVRAAFVGYVDPAK-----GMLPDPKNTIIVSWMIAQTVTAAGVVSYPEDTVRRM 238
Db      173 AIVGVGLPYVDITKRLILSGLMGDVYTHFLSSF-----TCGLAGALASNPVDVATRM 228
Qy      239 MMSG-RKGDIMTYGTVDCKRKIFRDEGKAFKGAANSVLR-GMGCAFVLVLYDELKK 296
Db      229 MNORVLADRGCSGYTGLDCLQTKWKEGFALYKGFMPWMLRLGPNWIIFFVYEQELKK 288
Qy      297 V 297
Db      289 L 289
```

```
RESULT 10
US-09-160-119-4
; Sequence 4, Application US/09160119A
; Patent No. 6316219
; GENERAL INFORMATION:
; APPLICANT: KRIEF, STEPHANE
; APPLICANT: SOUCHET, MICHEL
; APPLICANT: BRIL, ANTOINE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30985
; CURRENT APPLICATION NUMBER: US/09/160.119A
; CURRENT FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: EP 97402511.6
; EARLIER FILING DATE: 1997-10-23
; EARLIER APPLICATION NUMBER: EP 98401655.0
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 447
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-160-119-4
```

```
Query Match      18.1%; Score 280; DB 4; Length 447;
Best Local Similarity 27.1%; Pred. No. 5.1e-23;
Matches 80; Conservative 47; Mismatches 148; Indels 20; Gaps 6;

Qy      4 QAI SFADFLAGIAAISKTA VAPIERVKLLQVHASKQIADAKQYKGI VDCIVRI PK 63
Db      96 QVESA VRFGLGSVAGVATAVYPIDLVKTRM QNGSTGSFVGLMVKNSPDCFKVLR 155
Qy      64 EGVLSTWRGNLANVIRYPTQALNFAFKDKYKQIFL---GVDKHTQFMRYFAGNIASG 120
Db      156 YEGFGLYRGLLPOLLGVAPKAIKLTVNDPVRDKFMHKDGSVP-----LAAELIAG 207
Qy      121 GAAGATSLCFVYPLDPFARTRLAADVGKSGTEREFRGLDCLVKTIKSGTIGLVQGSFVS 180
Db      208 GCGGSGVITFNPLEIVKIRLQV-AGEITTGPRVSAL-----SVRDLGFFGIYKGAAC 261
Qy      181 VOGIIIRAAVFGVYDTAKGMLPDPKNTIIVSWMIAQTVTA V-AGVVSYPEDTVRRRM 239
Db      262 FLNDIPSAIYFPCYAHVKASFNEDQVSPGSLLAGALAGMPAASLVTPADVIKTR-- 319
Qy      240 MMSGRKADIMTYGTVDCKRKIFRDEGKAFKGAANSVLRGMGCAFVLVLYDEL 294
Db      320 LQVAAARAGQTTYSGVIDCFKRLIREBGPALMKAGARVFRSSPQFGVTILTYEL 374
```

```
RESULT 11
US-09-160-119-2
; Sequence 2, Application US/09160119A
; Patent No. 6316219
```

```
; GENERAL INFORMATION:
; APPLICANT: KRIEF, STEPHANE
; APPLICANT: SOUCHET, MICHEL
; APPLICANT: BRIL, ANTOINE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30985
; CURRENT APPLICATION NUMBER: US/09/160.119A
; CURRENT FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: EP 97402511.6
; EARLIER FILING DATE: 1997-10-23
; EARLIER APPLICATION NUMBER: EP 98401655.0
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 674
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-160-119-2
```

```
Query Match      18.1%; Score 280; DB 4; Length 674;
Best Local Similarity 27.1%; Pred. No. 9.4e-23;
Matches 80; Conservative 47; Mismatches 148; Indels 20; Gaps 6;

Qy      4 QAI SFADFLAGIAAISKTA VAPIERVKLLQVHASKQIADAKQYKGI VDCIVRI PK 63
Db      323 QVESA VRFGLGSVAGVATAVYPIDLVKTRM QNGSTGSFVGLMVKNSPDCFKVLR 382
Qy      64 EGVLSTWRGNLANVIRYPTQALNFAFKDKYKQIFL---GVDKHTQFMRYFAGNIASG 120
Db      383 YEGFGLYRGLLPOLLGVAPKAIKLTVNDPVRDKFMHKDGSVP-----LAAELIAG 434
Qy      121 GAAGATSLCFVYPLDPFARTRLAADVGKSGTEREFRGLDCLVKTIKSGTIGLVQGSFVS 180
Db      435 GCGGSGVITFNPLEIVKIRLQV-AGEITTGPRVSAL-----SVRDLGFFGIYKGAAC 488
Qy      181 VOGIIIRAAVFGVYDTAKGMLPDPKNTIIVSWMIAQTVTA V-AGVVSYPEDTVRRRM 239
Db      489 FLNDIPSAIYFPCYAHVKASFNEDQVSPGSLLAGALAGMPAASLVTPADVIKTR-- 546
Qy      240 MMSGRKADIMTYGTVDCKRKIFRDEGKAFKGAANSVLRGMGCAFVLVLYDEL 294
Db      547 LQVAAARAGQTTYSGVIDCFKRLIREBGPALMKAGARVFRSSPQFGVTILTYEL 601
```

```
RESULT 12
US-09-142-565-2
; Sequence 2, Application US/09142565A
; Patent No. 6187560
; GENERAL INFORMATION:
; APPLICANT: Lee James Beeley
; APPLICANT: Kelly, Patne
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30002
; CURRENT APPLICATION NUMBER: US/09/142.565A
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: 9704551.2
; EARLIER FILING DATE: 1997-03-05
; EARLIER APPLICATION NUMBER: 9705614.7
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: 97305305.1
; EARLIER FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
US-09-142-565-2
```

```
Query Match      17.2%; Score 265; DB 3; Length 312;
Best Local Similarity 27.1%; Pred. No. 1.5e-21;
```

Matches 82; Conservative 52; Mismatches 145; Indels 24; Gaps 8;

QY 7 SFAPKFLAGGIAAISKTAVERVIERVLLQVHASK--HASKQIADKQYKGIIVCIPIRPE 64  
 DB 12 TMAVVFELAGTACRADLVTFPLDTRAKVRLQIGESQGVRAVTAQVRGAVGTLTMTWRT 71  
 QY 65 QGVLSFWKGNLANVIRYFPTQALNFAFKDKYKQIFL-GGVDRHTQFWRYPAGNLASGGA 123  
 DB 72 EGPSPYNGVLVGLORQMSFASIRIGLYDSVKQVTPKADNSSLITRILA-----GCTT 126  
 QY 124 GATSLCFYVPLDPARTRLAADV--GKSGTEREFRGLGCLVKITSDGIRGLYOGFSVS 181  
 DB 127 GAMVATCAQPTDVVVRFOAQSIHLGPRSDRKYSGTMAVRIARBEGRGLMKGTLPVI 186  
 QY 182 QGIIIRAYAFGVYDTAKGMLPDPKXTHIVWSMIAQVTVA-----VAGVSYFPTDTR 236  
 DB 187 MRNALVNCALVETVITILEKLD---YHLLTNPFCHFVSARGAGFCATVAVSPDVVKT 243  
 QY 237 FMMQSGRKGADIMYGTVDCKRKIFRDEGKAFKGAWSNVL-R-GMGAFVLVLYDELK 295  
 DB 244 RYM-----NSPPQGYFSPLDCKIMVAGGPTAFYKGFPSFLRIGSMNVVVFVTEYDOLK 298  
 QY 296 KVI 298  
 DB 299 RAL 301

RESULT 13  
 US-08-518-878B-56  
 ; Sequence 56, Application US/08518878B  
 ; Patent No. 5702902  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tartaglia, Louis A.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
 ; TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY  
 ; NUMBER OF SEQUENCES: 57  
 ; CORRESPONDENCE ADDRESS:  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: U.S.A.  
 ; ZIP: 10036-2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/518,878B  
 ; FILING DATE: 23-AUG-1995  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Coruzzi, Laura A.  
 ; REGISTRATION NUMBER: 30,742  
 ; REFERENCE/DOCKET NUMBER: 7853-036  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-9741/8864  
 ; TELEX: 66141 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 56:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 299 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: unknown  
 ; US-08-518-878B-56

Query Match 16.2%; Score 250.5; DB 1; Length 299;  
 Best Local Similarity 24.9%; Pred. No. 6e-20;  
 Matches 74; Conservative 52; Mismatches 146; Indels 25; Gaps 8;

QY 12 FLAGGIAAISKTAVERVIERVLLQVHASK--QIADKQYKGIIVCIPIRPEQGV 68

DB 7 FLAGGTACIADLVTFPLDTRAKVRLQIGESQGVRAVTAQVRGAVGTLTMTWTEGPR 66  
 QY 69 SFMRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYPAGNLASGGAATSL 128  
 DB 67 SLVNGVLVGLORQMSFASVIRIGLYDSVKQFYTKG--SEHAS----IGSRLLAGSTTGALAV 121  
 QY 129 CFVYVPLDPARTRLAADVSGTEREFRGLGCLVKITSDGIRGLYOGFSVSVOGIIYR 188  
 DB 122 AVAQPTDVVVKRFOAQ-ARAGGRYOSTVNAVYRTIARBEGRGLMKGTSPVANAVALN 180  
 QY 189 AAYFGVYDTAK-----GMLPDPKXTHIVWSMIAQVTVAAGVVSYPFDTVRRMMQOS 242  
 DB 181 CABLVTVLIDALLKAMLMDBDLPCHTSAFGAGFCCTVIAS----PVDVVKIRYM--- 233  
 QY 243 GRKGADIMYGTVDCKRKIFRDEGKAFKGAWSNVL-R-GMGAFVLVLYDELKVI 298  
 DB 234 --NSALGOYSSAGHCALTMLQKEGPRAFYKGFMPSPFLRIGSMNVVVFVTEYDOLKRAL 288

RESULT 14  
 US-08-470-868A-56  
 ; Sequence 56, Application US/08470868A  
 ; Patent No. 5861485  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tartaglia, Louis C.  
 ; TITLE OF INVENTION: Compositions and Methods for the  
 ; Treatment of Body Weight Disorders, Including Obesity  
 ; NUMBER OF SEQUENCES: 56  
 ; CORRESPONDENCE ADDRESS:  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: IBM PC Compatible  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/470,868A  
 ; FILING DATE: 06-JUN-1995  
 ; CLASSIFICATION: 530  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Coruzzi, Laura A.  
 ; REGISTRATION NUMBER: 30,742  
 ; REFERENCE/DOCKET NUMBER: 7853-0031-999  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-8864  
 ; TELEX: 66441 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 56:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 299 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: unknown  
 ; US-08-470-868A-56

Query Match 16.2%; Score 250.5; DB 2; Length 299;  
 Best Local Similarity 24.9%; Pred. No. 6e-20;  
 Matches 74; Conservative 52; Mismatches 146; Indels 25; Gaps 8;

QY 12 FLAGGIAAISKTAVERVIERVLLQVHASK--QIADKQYKGIIVCIPIRPEQGV 68  
 DB 7 FLGAGTACIADLVTFPLDTRAKVRLQIGESQGVRAVTAQVRGAVGTLTMTWTEGPR 66  
 QY 69 SFMRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYPAGNLASGGAATSL 128  
 DB 67 SLVNGVLVGLORQMSFASVIRIGLYDSVKQFYTKG--SEHAS----IGSRLLAGSTTGALAV 121



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 18, 2003, 17:07:54 ; Search time 41 Seconds  
(without alignments)  
1153.671 Million cell updates/sec

Title: US-09-185-904A-33

Perfect score: 1543  
Sequence: 1 MTEQAISFANDFLAGIAAA.....LRGNGCAFLVLYDELKKVI 298

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues  
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*  
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*  
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*  
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*  
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*  
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1543	100.0	298	AAV71033	Human adenine nucl
2	1543	100.0	298	AAV71033	Human adenine nucl
3	1543	100.0	298	AAV71033	Human adenine nucl
4	1543	100.0	298	AAV71033	Human adenine nucl
5	1543	100.0	298	AAV71033	Human adenine nucl
6	1543	94.8	298	AAV71033	Human insulin rece
7	1543	94.2	298	AAV71033	Human adenine nucl
8	1543	94.2	298	AAV71033	Human adenine nucl
9	1543	94.2	298	AAV71033	Human adenine nucl

10	1418	91.9	429	24	ABR41715
11	1412	91.5	298	19	AAV6169
12	1406	91.1	293	22	ABU53219
13	1385.5	89.8	297	21	AAV71031
14	1385.5	89.8	297	22	AAU0198
15	1385.5	89.8	297	22	AAU0138
16	1367.5	88.6	325	22	ABG35423
17	1288	83.5	263	22	ABG37056
18	1254.5	81.3	299	22	ABR66082
19	1254.5	81.3	299	22	ABR67300
20	1137.5	73.7	307	22	ABR58380
21	1119	72.5	315	22	ABU53218
22	1119	72.5	315	22	ABR21175
23	1044	67.7	228	23	ABP43205
24	981	63.6	222	23	ABP74106
25	879.5	57.0	298	22	ABG18922
26	788.5	51.1	301	23	ABP73357
27	763	49.4	484	22	ABG15422
28	763	49.4	484	22	ABG37055
29	749.5	48.6	386	22	AAV00106
30	743	48.2	379	24	ABR81267
31	742.5	48.1	346	21	AAV65577
32	742.5	48.1	346	21	AAV37261
33	742.5	48.1	346	21	AAV37264
34	742.5	48.1	346	21	AAV38460
35	742.5	48.1	363	21	AAV36576
36	742.5	48.1	363	21	AAV37260
37	742.5	48.1	363	21	AAV37263
38	742.5	48.1	363	21	AAV38459
39	742.5	48.1	381	21	AAV36575
40	742.5	48.1	381	21	AAV37259
41	742.5	48.1	381	21	AAV37262
42	742.5	48.1	381	21	AAV38465
43	742.5	48.1	392	21	AAV38672
44	742.5	48.1	1009	21	AAV38671
45	742.5	48.1	1027	21	AAV38670

## ALIGNMENTS

RESULT 1  
AAV71033  
ID AAV71033 standard; Protein: 298 AA.

AAV71033;

29-AUG-2000 (first entry)

Human adenine nucleotide translocator ANT3.

Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;  
adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;  
mitochondrial permeability transition; neuroprotective; nocrotic;  
antiParkinsonian; cytoleptic; antidiabetic; anticonvulsant; neuroleptic;  
antiparkinsonian; cerebroprotective; therapeutic; screening; psoriasis;  
Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;  
diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;  
mitochondrial encephalopathy; lactic acidosis; stroke; MIDP;  
mitochondrial diabetes and deafness; hyperproliferative disorder;  
myoclonic epilepsy red ragged fibre syndrome.

Homo sapiens.

MO200026370-A2.

11-MAY-2000.

03-NOV-1999; 99MO-US25883.

03-NOV-1998; 98US-0185904.

08-SEP-1999; 99US-0393441.

PA (MITO-) MITOKOR.  
 XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;  
 PI Ghosh SS;  
 XX WPI; 2000-365619/31.  
 DR N-PSDB; AAD00521.  
 XX  
 PT Recombinant construct encoding adenine nucleotide translocator  
 PT polypeptide, useful e.g. in screening for potential therapeutic agents  
 PT against mitochondrial disease -  
 XX  
 PS Claim 46; Page 173-174; 175pp; English.  
 XX  
 CC The patent discloses a method to produce adenine nucleotide translocator  
 CC (ANT) proteins or ANT fusion proteins using recombinant expression  
 CC constructs. ANT is a nuclear encoded protein and a major component of  
 CC inner mitochondrial membrane. It mediates transport of adenosine  
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves  
 CC as an important molecular component of the mitochondrial permeability  
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents  
 CC or ligands that bind to, or interact with it. The ANT ligands are used to  
 CC detect or isolate ANT in a biological sample, and therapeutically for  
 CC regulating mitochondrial pore activity, for treating diseases associated  
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's  
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,  
 CC Deber's hereditary optic neuropathy, schizophrenia, mitochondrial  
 CC cephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative  
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic  
 CC epilepsy red ragged fibre syndrome. The present sequence is an  
 CC adenine nucleotide translocator ANT3 from human brain.  
 XX  
 SQ Sequence 298 AA;

Query Match 100.0%; Score 1543; DB 21; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 4,6e-157;  
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MTEQATSPAKDPLAGGIAAISTKTAAPIERVLLQOVHASQIADKQYKGIIVCTIVR 60  
 DB 1 MTEQATSPAKDPLAGGIAAISTKTAAPIERVLLQOVHASQIADKQYKGIIVCTIVR 60  
 QY 61 IPKEQGLSPFRGNLANVIRYPTQALNFAFKQYKQIFLGVDKHTQFRYRAGNLSAG 120  
 DB 61 IPKEQGLSPFRGNLANVIRYPTQALNFAFKQYKQIFLGVDKHTQFRYRAGNLSAG 120  
 QY 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFRGLGDCLVKITSDGIRGLYQGFSSV 180  
 DB 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFRGLGDCLVKITSDGIRGLYQGFSSV 180  
 QY 181 VQGIITIRAYRPGVYDTAKMLPDPKNTHTVSWMTAQVTAAGVSYFPDVRRRMM 240  
 DB 181 VQGIITIRAYRPGVYDTAKMLPDPKNTHTVSWMTAQVTAAGVSYFPDVRRRMM 240  
 QY 241 QSGRKGADIMYTGTVDCKRKIFRDEGKAFKGMASNVLMGGAFAVLVYDELKKVI 298  
 DB 241 QSGRKGADIMYTGTVDCKRKIFRDEGKAFKGMASNVLMGGAFAVLVYDELKKVI 298

RESULT 2  
 AAM39641  
 ID AAM39641 standard; Protein; 298 AA.  
 XX  
 AC AAM39641;  
 XX  
 DT 22-OCT-2001 (first entry)  
 XX  
 DE Human polypeptide SEQ ID NO 2786.  
 XX  
 KW Human; nootropic; immunosuppressant; cyostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KM leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200153312-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 26-DEC-2000; 2000MO-US34263.  
 XX  
 PR 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 09-JUL-2000; 2000US-0598042.  
 PR 19-JUL-2000; 2000US-0620312.  
 PR 03-AUG-2000; 2000US-0653450.  
 PR 14-SEP-2000; 2000US-0662191.  
 PR 19-OCT-2000; 2000US-0693036.  
 PR 29-NOV-2000; 2000US-0727344.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PT Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PT Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
 XX  
 DR WPI; 2001-442253/47.  
 DR N-PSDB; AAI58797.  
 XX  
 PT Novel nucleic acids and polypeptides, useful for treating disorders  
 PT such as central nervous system injuries -  
 XX  
 PS Example 4; SEQ ID NO 2786; 10078pp; English.

The invention relates to human nucleic acids (AA157798-AA161369) and  
 the encoded polypeptides (AAM38642-AAM42213) with nootropic,  
 immunosuppressant and cyostatic activity. The polynucleotides are useful  
 in gene therapy. A composition containing a polypeptide or polynucleotide  
 of the invention may be used to treat diseases of the peripheral nervous  
 system, such as peripheral nervous injuries, peripheral neuropathy and  
 localised neuropathies and central nervous system diseases, such as  
 Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 utilisation of the activities such as: Immune system suppression,  
 CC activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemia and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.  
 XX  
 SQ Sequence 298 AA;

Query Match 100.0%; Score 1543; DB 22; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 4,6e-157;  
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MTEQATSPAKDPLAGGIAAISTKTAAPIERVLLQOVHASQIADKQYKGIIVCTIVR 60  
 DB 1 MTEQATSPAKDPLAGGIAAISTKTAAPIERVLLQOVHASQIADKQYKGIIVCTIVR 60  
 QY 61 IPKEQGLSPFRGNLANVIRYPTQALNFAFKQYKQIFLGVDKHTQFRYRAGNLSAG 120  
 DB 61 IPKEQGLSPFRGNLANVIRYPTQALNFAFKQYKQIFLGVDKHTQFRYRAGNLSAG 120  
 QY 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFRGLGDCLVKITSDGIRGLYQGFSSV 180  
 DB 121 GAAGATSLCFVYPLDFAKRLADVKGSGTEREFRGLGDCLVKITSDGIRGLYQGFSSV 180  
 QY 181 VQGIITIRAYRPGVYDTAKMLPDPKNTHTVSWMTAQVTAAGVSYFPDVRRRMM 240  
 DB 181 VQGIITIRAYRPGVYDTAKMLPDPKNTHTVSWMTAQVTAAGVSYFPDVRRRMM 240  
 QY 241 QSGRKGADIMYTGTVDCKRKIFRDEGKAFKGMASNVLMGGAFAVLVYDELKKVI 298  
 DB 241 QSGRKGADIMYTGTVDCKRKIFRDEGKAFKGMASNVLMGGAFAVLVYDELKKVI 298



Qy 241 QSGRGADIMYTGVDWCWKIFRDEGGKAFKFGAMSNVLRGMGAFVLVYDELKKVI 298  
 Db 241 QSGRGADIMYTGVDWCWKIFRDEGGKAFKFGAMSNVLRGMGAFVLVYDELKKVI 298

RESULT 3  
 AAU01200  
 ID AAU01200 standard; Protein; 298 AA.  
 AC AAU01200;  
 XX  
 XX 07-SEP-2001 (first entry)  
 DE Human adenine nucleotide translocator-3 (ANT-3) protein.  
 KW Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;  
 KW mitochondrial permeability transition pore component; cell survival;  
 KW mitochondrial core component; mitochondrial related disorder; cancer;  
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.  
 XX  
 OS Homo sapiens.  
 XX WO200132876-A2.  
 PN 10-MAY-2001.  
 PD 03-NOV-2000; 2000WO-US30535.  
 PE 03-NOV-1999; 99US-0434354.  
 PR (MITO-) MITOKOR.  
 XX  
 PA Murphy AN, Clevenger W, Wiley SE, Andreyev AV, Frigeri LG;  
 PI Velicelcebi G, Davis RE;  
 PI N-PSDB; AAS05903.  
 DR WPI; 2001-291054/30.  
 XX  
 XX \*New nucleic acid expression constructs, useful for screening for agents  
 PT that alter mitochondrial permeability transition (MPT), comprises  
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide  
 PT fused to energy transfer molecule -  
 PS Disclosure; Fig 2; 186pp; English.

XX The present sequence represents human adenine nucleotide translocator-3  
 CC (ANT-3) protein. ANT proteins are mitochondrial permeability  
 CC transition (MTP) pore components responsible for mediating transport  
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact  
 CC with other mitochondrial core components e.g. cyclophilins to  
 CC regulate MPT. The present invention relates to a novel nucleic acid  
 CC expression construct comprising a promoter operably linked to a  
 CC polynucleotide encoding a mitochondrial pore component polypeptide  
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein  
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel  
 CC expression construct can alter mitochondrial membrane permeability  
 CC transition and/or alter the interaction between mitochondrial core  
 CC components. The methods are useful for screening for agents that alter  
 CC MPT and/or cell survival. These agents are useful for the prevention or  
 CC treatment of diseases associated with altered mitochondrial function or  
 CC dysfunction of cell survival, such as Alzheimer's disease, diabetes  
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,  
 CC mitochondrial encephalopathy, lactic acidosis, stroke,  
 CC hyperproliferative disorders e.g. cancer, and deathness.

XX  
 SQ Sequence 298 AA;  
 Query Match 100.0%; Score 1543; DB 22; Length 298;  
 Best Local Similarity 100.0%; Pred. NO. 4.6e-157;  
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLQVOHASKQIADKQYKIVDCIVR 60  
 |||

Db 1 MTEQAISFAKDFLAGGIAAAISKTAVAPIERVKLLQVOHASKQIADKQYKIVDCIVR 60  
 Qy 61 IPEKGVLSFMRGNANVIRYFPQALNFAFKDKYKQIFLGVDHGTQFMYFAGNLASG 120  
 Db 61 IPEKGVLSFMRGNANVIRYFPQALNFAFKDKYKQIFLGVDHGTQFMYFAGNLASG 120  
 Qy 121 GAAGATSLCFYVPLDFARTRLAADVGSKGTREBERGLGDCIWKITKSDGIRGLYQGFSSVS 180  
 Db 121 GAAGATSLCFYVPLDFARTRLAADVGSKGTREBERGLGDCIWKITKSDGIRGLYQGFSSVS 180  
 Qy 181 VQGIITRYAAVFGYVDTAKGMLPDPKNTHTIVSNMIAQTVAVGVSSYPEDTVRRMM 240  
 Db 181 VQGIITRYAAVFGYVDTAKGMLPDPKNTHTIVSNMIAQTVAVGVSSYPEDTVRRMM 240

Qy 241 QSGRGADIMYTGVDWCWKIFRDEGGKAFKFGAMSNVLRGMGAFVLVYDELKKVI 298  
 Db 241 QSGRGADIMYTGVDWCWKIFRDEGGKAFKFGAMSNVLRGMGAFVLVYDELKKVI 298

RESULT 4  
 AAU10380  
 ID AAU10380 standard; Protein; 298 AA.  
 AC AAU10380;  
 XX  
 XX 14-FEB-2002 (first entry)  
 DE Human adenine nucleotide translocator 3 (ANT3).  
 KW Human; adenine nucleotide translocator; ANT;  
 KW mitochondrial matrix protein.  
 XX  
 OS Homo sapiens.  
 XX WO200185944-A2.  
 PN 15-NOV-2001.  
 PD 11-MAY-2001; 2001WO-US15416.  
 PE 11-MAY-2000; 2000US-0569327.  
 PR (MITO-) MITOKOR.  
 XX  
 PA Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;  
 PI Ghosh SS, Moos WH, Pei Y, Carroll AK;  
 PI N-PSDB; AAS16690.  
 DR WPI; 2002-055598/07.  
 XX  
 XX Novel recombinant expression construct for producing adenine nucleotide  
 PT translocator polypeptides, comprises a regulated promoter linked to  
 PT nucleic acid encoding the polypeptide -  
 PS Example 3; Fig 2; 147pp; English.

XX The invention relates to a recombinant expression construct (I)  
 CC comprising a regulated promoter operably linked to a nucleic acid  
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT  
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial  
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant  
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and  
 CC culturing the host cell. (I) is also useful for targeting a polypeptide  
 CC of interest to a mitochondrial membrane, where ANT polypeptide is  
 CC expressed as a fusion protein with the polypeptide of interest.  
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is  
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT  
 CC ligand is useful for determining the presence of an ANT polypeptide,  
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating  
 CC ANT from a biological sample, where the ANT ligand is covalently or non-  
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also  
 CC useful for identifying an agent that interacts with an ANT polypeptide.  
 CC The present sequence represents the amino acid sequence of human ANT3.

```

XX Sequence 298 AA;
SQ
Query Match 100.0%; Score 1543; DB 23; Length 298;
Best Local Similarity 100.0%; Pred. No. 4,6e-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQALSPAKDFLAGGIAAISTKAVAPIERVKLLQVQASKOIADKQYKGIIVDCIVR 60
DB 1 MTEQALSPAKDFLAGGIAAISTKAVAPIERVKLLQVQASKOIADKQYKGIIVDCIVR 60
QY 61 IPKEQGLSPFRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLASG 120
DB 61 IPKEQGLSPFRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLASG 120
QY 121 GAAGATSLCFVYPLDPAKTRTLADVGSKSTEREFRGLDCLVKTSDGIRGLYQGSVS 180
DB 121 GAAGATSLCFVYPLDPAKTRTLADVGSKSTEREFRGLDCLVKTSDGIRGLYQGSVS 180
QY 181 VGGIITRAAYFGVYDTAKGMLPDPKXNTHIVSMWIAQTVAAGVVSYPEDTVRRMM 240
DB 181 VGGIITRAAYFGVYDTAKGMLPDPKXNTHIVSMWIAQTVAAGVVSYPEDTVRRMM 240
QY 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFFKGAMSVLRMGCAFVLVLYDELKQYI 298
DB 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFFKGAMSVLRMGCAFVLVLYDELKQYI 298

RESULT 5
AAM41427
ID AAM41427 standard; Protein; 323 AA.
AC AAM41427;
DT 22-OCT-2001 (first entry)
DE Human polypeptide SEQ ID NO 6358.
XX
XX Human; neurotrophic; immunosuppressant; cytoskeletal; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia.
XX
XX Homo sapiens.
XX
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US34263.
XX
XX 21-JAN-2000; 2000US-0488725.
XX
XX 25-APR-2000; 2000US-0552317.
XX
XX 09-JUL-2000; 2000US-0598042.
XX
XX 19-JUL-2000; 2000US-0620312.
XX
XX 03-AUG-2000; 2000US-0653450.
XX
XX 14-SEP-2000; 2000US-0662191.
XX
XX 19-OCT-2000; 2000US-0693036.
XX
XX 29-NOV-2000; 2000US-0727344.
XX
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AB, Yang Y, Zhang J;
XX Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI, 2001-442253/47.
XX
XX N-PSDB; AAI60583.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
XX such as central nervous system injuries -

```

```

XX
XX Example 2; SEQ ID NO 6358; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and
XX the encoded polypeptides (AAM38642-AAM42213) with neurotrophic,
XX immunosuppressant and cytoskeletal activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: Immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukaemias and
XX C.N.S disorders.
XX Note: The sequence data for this patent did not form part of the printed
XX specification.
XX
XX Sequence 323 AA;
SQ
Query Match 100.0%; Score 1543; DB 22; Length 323;
Best Local Similarity 100.0%; Pred. No. 5,2e-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQALSPAKDFLAGGIAAISTKAVAPIERVKLLQVQASKOIADKQYKGIIVDCIVR 60
DB 26 MTEQALSPAKDFLAGGIAAISTKAVAPIERVKLLQVQASKOIADKQYKGIIVDCIVR 85
QY 61 IPKEQGLSPFRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLASG 120
DB 86 IPKEQGLSPFRGNLANVIRFPPTQALNFAFKDKYKQIFLGVDKHTQFMRYPAGNLASG 145
QY 121 GAAGATSLCFVYPLDPAKTRTLADVGSKSTEREFRGLDCLVKTSDGIRGLYQGSVS 180
DB 146 GAAGATSLCFVYPLDPAKTRTLADVGSKSTEREFRGLDCLVKTSDGIRGLYQGSVS 205
QY 181 VGGIITRAAYFGVYDTAKGMLPDPKXNTHIVSMWIAQTVAAGVVSYPEDTVRRMM 240
DB 206 VGGIITRAAYFGVYDTAKGMLPDPKXNTHIVSMWIAQTVAAGVVSYPEDTVRRMM 265
QY 241 QSGRKGADIMYTGTVDCWRKIFRDEGKAFFKGAMSVLRMGCAFVLVLYDELKQYI 298
DB 266 QSGRKGADIMYTGTVDCWRKIFRDEGKAFFKGAMSVLRMGCAFVLVLYDELKQYI 323

RESULT 6
AAO18516
ID AAO18516 standard; Protein; 298 AA.
XX
XX AAO18516;
XX
XX 11-OCT-2002 (first entry)
XX
XX Human insulin receptor signaling modifier SEQ ID NO: 54.
XX
XX Human; insulin receptor signaling; insulin receptor signaling modifier;
XX IEM; diabetes; metabolic syndrome; antidiabetic.
XX
XX Homo sapiens.
XX
XX WO200255664-A2.
XX
XX 18-JUL-2002.
XX
XX 11-JAN-2002; 2002WO-US01048.
XX
XX 12-JAN-2001; 2001US-261226P.
XX
XX 12-JAN-2001; 2001US-261303P.
XX
XX 12-JAN-2001; 2001US-261304P.
XX
XX 12-JAN-2001; 2001US-261335P.
XX
XX 12-JAN-2001; 2001US-261336P.

```

PR 12-JAN-2001; 2001US-261361P.  
PR 12-JAN-2001; 2001US-261456P.  
PR 12-JAN-2001; 2001US-261456P.  
PR 12-JAN-2001; 2001US-261458P.  
PR 12-JAN-2001; 2001US-261459P.  
PR 12-JAN-2001; 2001US-261461P.  
PR 12-JAN-2001; 2001US-261518P.  
PR 12-JAN-2001; 2001US-261531P.  
PR 12-JAN-2001; 2001US-261532P.  
PR 12-JAN-2001; 2001US-261589P.  
PR 12-JAN-2001; 2001US-261590P.  
PR 12-JAN-2001; 2001US-261694P.  
PR 12-JAN-2001; 2001US-261695P.  
PR 12-JAN-2001; 2001US-261697P.  
XX  
XX (EXEL-) EXELIXIS INC.  
XX  
XX Seidel-Dugan C, Ferguson KC, Kidd T,  
XX  
XX WPI; 2002-599664/64.  
XX  
XX N-PSDB; AAL46635.  
XX  
XX Identifying an insulin receptor signaling modulator, useful as drug  
XX targets for treating diabetes or metabolic disorders, comprises  
XX contacting an assay system comprising insulin receptor signaling  
XX modifiers with a test agent -  
XX  
XX  
XX Disclosure; Page 160-161; 232pp; English.  
XX  
XX The present invention relates to a method of identifying a candidate  
XX insulin receptor (INR) signaling modulating agent, involving contacting  
XX an assay system comprising an insulin receptor signaling modifier (ISM)  
XX polypeptide or nucleic acid with a test agent, and detecting a test  
XX agent-biased activity of the assay system. The method is useful for  
XX identifying candidate INR signaling modulating agents. ISM genes may be  
XX used as drug targets for treatment of disorders related to INR signaling  
XX such as diabetes or metabolic syndrome. ISM nucleic acids and  
XX polypeptides are useful for identifying and testing agents that modulate  
XX ISM function and for other applications related to the involvement of ISM  
XX in INR signaling, and for identifying subjects having a predisposition to  
XX such diseases associated with INR signaling. The present sequence is an  
XX ISM protein described in the exemplification of the invention.  
XX  
XX Sequence 298 AA:  
SQ  
Query Match 94.8%; Score 1463; DB 23; Length 298;  
Best Local Similarity 92.9%; Pred. No. 1.8e-148;  
Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;  
QY 1 MTEQALSFADKFLAGGIAAISTAVAPIERVKLLQVQHSKQIADKQYKGIYDCIVR 60  
DB 1 MTDAAVSAKDFLAGGVAALSKTAVAPIERVKLLQVQHSKQITADKQYKGIIDCVVR 60  
QY 61 IPKEGVLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120  
DB 61 IPKEGVLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120  
QY 121 GAAGATSLCFYRPPDFASTRLLADYKSGTEFEFGDCLVYTKSGICRGLYGGSEVS 180  
DB 121 GAAGATSLCFYRPPDFASTRLLADYKSGTEFEFGDCLVYTKSGICRGLYGGSEVS 180  
QY 121 GAAGATSLCFYRPPDFASTRLLADYKSGTEFEFGDCLVYTKSGICRGLYGGSEVS 180  
DB 121 GAAGATSLCFYRPPDFASTRLLADYKSGTEFEFGDCLVYTKSGICRGLYGGSEVS 180  
QY 181 VGGIITVAAVFGVYDTPAKGMLPDKNTHIVVSMIAQTVAVAVVSPPTVARRMM 240  
DB 181 VGGIITVAAVFGVYDTPAKGMLPDKNTHIVVSMIAQTVAVAVVSPPTVARRMM 240  
QY 241 QSGRGADIMTYGIVDCWRKIFRDEGGAFFKGAWSNVLRGGAFFVLVYDELK 296  
DB 241 QSGRGADIMTYGIVDCWRKIFRDEGGAFFKGAWSNVLRGGAFFVLVYDELK 296  
RESULT 7  
AAV71032 standard; Protein; 298 AA.

XX  
AC AAY71032;  
XX  
XX 29-AUG-2000 (first entry)  
DT  
XX Human adenine nucleotide translocator ANT2.  
XX  
XX Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;  
XX adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;  
XX mitochondrial permeability transition; neuroprotective; neurotropic;  
XX antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;  
XX antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;  
XX Alzheimer's disease; Parkinson's disease; Huntington's disease; dyctonia;  
XX diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;  
XX mitochondrial encephalopathy; lactic acidosis; stroke; MTD;  
XX mitochondrial diabetes and deafness; hyperproliferative disorder;  
XX myoclonic epilepsy red ragged fibre syndrome.  
XX  
XX Homo sapiens.  
XX  
XX WO200026370-A2.  
XX  
XX 11-MAY-2000.  
XX  
XX 03-NOV-1999; 99WO-US25883.  
XX  
XX 03-NOV-1998; 98US-0185904.  
XX  
XX 08-SEP-1999; 99US-0393441.  
XX  
XX (MITO-) MITOKOR.  
XX  
XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR,  
XX Ghosh SS;  
XX WPI; 2000-365619/31.  
XX  
XX N-PSDB; AAD00520.  
XX  
XX Recombinant construct encoding adenine nucleotide translocator  
XX polypeptide, useful e.g. in screening for potential therapeutic agents  
XX against mitochondrial disease -  
XX  
XX  
XX Claim 45; Page 172-173; 175pp; English.  
XX  
XX The patent discloses a method to produce adenine nucleotide translocator  
XX (ANT) proteins or ANT fusion proteins using recombinant expression  
XX constructs. ANT is a nuclear encoded protein and a major component of  
XX inner mitochondrial membrane. It mediates transport of adenosine  
XX di/tri-phosphates across the mitochondrial inner membrane and also serves  
XX as an important molecular component of the mitochondrial permeability  
XX transition pore, a modulator of apoptosis. ANT is used to identify agents  
XX or ligands that bind to, or interact with it. The ANT ligands are used to  
XX detect or isolate ANT in a biological sample, and therapeutically for  
XX regulating mitochondrial pore activity, for treating diseases associated  
XX with altered mitochondrial function, including Alzheimer's, Parkinson's  
XX and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,  
XX Leber's hereditary optic neuropathy, schizophrenia, mitochondrial  
XX encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative  
XX disorders, mitochondrial diabetes and deafness (MTD), and myoclonic  
XX epilepsy red ragged fibre syndrome. The present sequence is an  
XX adenine nucleotide translocator ANT2 from human brain.  
XX  
XX Sequence 298 AA;  
SQ  
Query Match 94.2%; Score 1454; DB 21; Length 298;  
Best Local Similarity 92.6%; Pred. No. 1.7e-147;  
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;  
QY 1 MTEQALSFADKFLAGGIAAISTAVAPIERVKLLQVQHSKQIADKQYKGIYDCIVR 60  
DB 1 MTDAAVSAKDFLAGGVAALSKTAVAPIERVKLLQVQHSKQITADKQYKGIIDCVVR 60  
QY 61 IPKEGVLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120  
DB 61 IPKEGVLSPFRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120

Db 61 IPKEQVLSEFWRGNLANVIRYPTQALNFAFKKXKQIFLGVDKRTQFWRYPAGNLASG 120  
 Qy 121 GAAGATSLCFVYPLDFAFRTLRADVGKSGTEREFGDGLVKTSDGIRGLYQGSFVS 180  
 Db 121 GAAGATSLCFVYPLDFAFRTLRADVGKSGTEREFGDGLVKTSDGIRGLYQGSFVS 180  
 Qy 181 VGGIITRYAAVFGVYDTAKGMLPDPKNTHTIVSMIAQTVAAGVVSYPFDVRRMM 240  
 Db 181 VGGIITRYAAVFGVYDTAKGMLPDPKNTHTIVSMIAQTVAAGVVSYPFDVRRMM 240  
 Qy 241 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFKGAWSNVLKMGGAFLVLYDELK 296  
 Db 241 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFKGAWSNVLKMGGAFLVLYDELK 296  
 RESULT 8  
 AAU01199 standard; Protein: 298 AA.  
 AC AAU01199;  
 DT 07-SEP-2001 (first entry)  
 DE Human adenine nucleotide translocator-2 (ANT-2) protein.  
 XX Human, adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;  
 KM mitochondrial permeability transition pore component; cell survival;  
 KM mitochondrial core component; mitochondrial related disorder; cancer;  
 KM Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.  
 OS Homo sapiens.  
 PN WO200132876-A2.  
 PD 10-MAY-2001.  
 PF 03-NOV-2000; 2000WO-US30535.  
 PR 03-NOV-1999; 99US-0434354.  
 PA (MITO-) MITOKOR.  
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;  
 PI Velicelcibi G, Davis RE;  
 DR WPI: 2001-2291054/30.  
 DR N-PSDB; AAS05902.  
 PT New nucleic acid expression constructs, useful for screening for agents  
 PT that alter mitochondrial permeability transition (MPT), comprises  
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide  
 PT fused to energy transfer molecule -  
 PS Disclosure; Fig 2; 186pp; English.  
 XX The present sequence represents human adenine nucleotide translocator-2  
 CC (ANT-2) protein. ANT proteins are mitochondrial permeability  
 CC translocation (MTP) pore components responsible for mediating transport  
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact  
 CC with other mitochondrial core components e.g. cyclophilins to  
 CC regulate MPT. The present invention relates to a novel nucleic acid  
 CC expression construct comprising a promoter operably linked to a  
 CC polynucleotide encoding a mitochondrial pore component polypeptide  
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein  
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel  
 CC expression construct can alter mitochondrial membrane permeability  
 CC translocation and/or alter the interaction between mitochondrial core  
 CC components. The methods are useful for screening for agents that alter  
 CC MPT and/or cell survival. These agents are useful for the prevention or  
 CC treatment of diseases associated with altered mitochondrial function or  
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes  
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,  
 CC mitochondrial encephalopathy, lactic acidosis, stroke,

CC hyperproliferative disorders e.g. cancer, and deafness.  
 XX Sequence 298 AA;  
 Query Match 94.2%; Score 1454; DB 22; Length 298;  
 Best Local Similarity 92.6%; Pred. No. 1.7e-147;  
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;  
 Qy 1 MTEQALSFADPFLAGIAAIAISKTAIVAPIRRVKLLLOVQASKOITADKQYKGIIVDCIVR 60  
 Db 1 MTDALSFADPFLAGIAAIAISKTAIVAPIRRVKLLLOVQASKOITADKQYKGIIVDCIVR 60  
 Qy 61 IPKEQVLSEFWRGNLANVIRYPTQALNFAFKKXKQIFLGVDKRTQFWRYPAGNLASG 120  
 Db 61 IPKEQVLSEFWRGNLANVIRYPTQALNFAFKKXKQIFLGVDKRTQFWRYPAGNLASG 120  
 Qy 121 GAAGATSLCFVYPLDFAFRTLRADVGKSGTEREFGDGLVKTSDGIRGLYQGSFVS 180  
 Db 121 GAAGATSLCFVYPLDFAFRTLRADVGKSGTEREFGDGLVKTSDGIRGLYQGSFVS 180  
 Qy 181 VGGIITRYAAVFGVYDTAKGMLPDPKNTHTIVSMIAQTVAAGVVSYPFDVRRMM 240  
 Db 181 VGGIITRYAAVFGVYDTAKGMLPDPKNTHTIVSMIAQTVAAGVVSYPFDVRRMM 240  
 Qy 241 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFKGAWSNVLKMGGAFLVLYDELK 296  
 Db 241 QSGRKGADIMYTGTVDCWRKIFRDEGGKAFKGAWSNVLKMGGAFLVLYDELK 296  
 RESULT 9  
 AAU01379 standard; Protein: 298 AA.  
 AC AAU01379;  
 DT 14-FEB-2002 (first entry)  
 DE Human adenine nucleotide translocator 2 (ANT2).  
 XX Human, adenine nucleotide translocator; ANT; ss;  
 KM mitochondrial matrix protein.  
 OS Homo sapiens.  
 PN WO200185944-A2.  
 PD 15-NOV-2001.  
 PF 11-MAY-2001; 2001WO-US15416.  
 PR 11-MAY-2000; 2000US-0569327.  
 PA (MITO-) MITOKOR.  
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;  
 PI Ghosh SS, Moos WH, Pei Y, Carroll AK;  
 DR WPI: 2002-055598/07.  
 DR N-PSDB; AAS16689.  
 PT Novel recombinant expression construct for producing adenine nucleotide  
 PT translocator polypeptides, comprises a regulated promoter linked to  
 PT nucleic acid encoding the polypeptide -  
 PS Claim 44; Fig 2; 147pp; English.  
 XX The invention relates to a recombinant expression construct (I)  
 CC comprising a regulated promoter operably linked to a nucleic acid  
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT  
 CC proteins mediate the exchange of ADP synthesised in the mitochondrial  
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant  
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and  
 CC culturing the host cell. (I) is also useful for targeting a polypeptide

CC of interest to a mitochondrial membrane, where ANT polypeptide is  
 CC expressed as a fusion protein with the polypeptide of interest.  
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is  
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT  
 CC ligand is useful for determining the presence of an ANT polypeptide.  
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating  
 CC ANT from a biological sample, where the ANT ligand is covalently or non-  
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also  
 CC useful for identifying an agent that interacts with an ANT polypeptide.  
 CC The present sequence represents the amino acid sequence of human ANT2.  
 XX  
 SQ Sequence 298 AA;  
 Query Match 94.2%; Score 1454; DB 23; Length 298;  
 Best Local Similarity 92.6%; Pred. No. 1.7e-147;  
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 MTEQAISFAKDFLAGIAAIAISKTAVPIERVKLLQVQHASKQIADKQYGVDCIVR 60  
 DB 1 MTDALSFPAKDFLAGIAAIAISKTAVPIERVKLLQVQHASKQIADKQYGVDCIVR 60  
 QY 61 IPKEQGVLSFWRGNLANVIRFPQALNFAFDKTKQIFLGVDKHTQFWRFAGNLASG 120  
 DB 61 IPKEQGVLSFWRGNLANVIRFPQALNFAFDKTKQIFLGVDKHTQFWRFAGNLASG 120  
 QY 121 GAAAGTSLCFYVPLDPFARTRLAADVSGTEREERGLGDCIVKTKSGIRGLYQGFVS 180  
 DB 121 GAAAGTSLCFYVPLDPFARTRLAADVSGTEREERGLGDCIVKTKSGIRGLYQGFVS 180  
 QY 181 VOGIIITRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQTVTAAGVSYPPDVTARRMM 240  
 DB 181 VOGIIITRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQTVTAAGVSYPPDVTARRMM 240  
 QY 241 OSGRKADIMTGTVDCKRKIFRDGCGAFAFGANSVLRMGAFVLVLDLKK 296  
 DB 241 OSGRKADIMTGTVDCKRKIFRDGCGAFAFGANSVLRMGAFVLVLDLKK 296  
 DB 241 OSGRKADIMTGTVDCKRKIFRDGCGAFAFGANSVLRMGAFVLVLDLKK 296  
 Result 10  
 ABR41715  
 ID ABR41715 standard; Protein; 429 AA.  
 XX  
 AC ABR41715;  
 XX  
 DT 02-JUN-2003 (first entry)  
 XX  
 DE Human DITHP organelle-associated protein.  
 XX  
 KW Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;  
 KW cancer; cell proliferative disorder; autoimmune disorder;  
 KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;  
 KW neurological disorder; gastrointestinal disorder; transport disorder;  
 KW connective tissue disorder; drug screening; proteome analysis;  
 KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;  
 KW disease model; toxicological testing; transcript imaging;  
 KW organelle-associated protein.  
 KW  
 OS Homo sapiens.  
 XX  
 XX WO200297031-A2.  
 XX  
 PD 05-DEC-2002.  
 XX  
 PF 27-MAR-2002; 2002WO-US10056.  
 XX  
 XX 28-MAR-2001; 2001US-279619P.  
 PR 29-MAR-2001; 2001US-280067P.  
 PR 29-MAR-2001; 2001US-280068P.  
 PR 16-MAY-2001; 2001US-291280P.  
 PR 17-MAY-2001; 2001US-291829P.  
 PR 17-MAY-2001; 2001US-291849P.  
 PR 19-JUN-2001; 2001US-299428P.  
 PR 20-JUN-2001; 2001US-299776P.

PR 20-JUN-2001; 2001US-300001P.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amesley SR;  
 PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleeefeld Y, Gerstin EH;  
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
 PI Flores V, Marwaha R, Lo A, Lan RX, Urashka ME;  
 XX  
 DR WPI; 2003-129518/12.  
 DR N-PSDB; ACC46652.  
 XX  
 PT Novel human diagnostic and therapeutic polypeptide useful for  
 PT identifying test compound which specifically binds to a polypeptide  
 PT encoded by human diagnostic and therapeutic polynucleotide, and to  
 PT induce antibodies  
 XX  
 PS Claim 27; SEQ ID No 1250; 591pp; English.  
 XX  
 CC The invention relates to novel human diagnostic and therapeutic  
 CC polynucleotides designated dithp (ACC46080-ACC46749) and to their  
 CC encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates  
 CC to polynucleotide sequences at least 90% identical to the dithp CDNA  
 CC sequences of the invention; recombinant vectors, host cells and  
 CC transgenic organisms comprising a dithp nucleic acid sequence; the  
 CC recombinant production of DITHP proteins; antibodies specific for DITHP  
 CC proteins; microarrays comprising dithp nucleic acid sequences; methods  
 CC of detecting dithp nucleotide and protein sequences; methods of screening  
 CC for compounds which specifically bind a DITHP protein; and methods of  
 CC assessing the toxicity of test compounds using a dithp hybridisation  
 CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the  
 CC diagnosis of a wide variety of conditions including cancer and other cell  
 CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,  
 CC viral, fungal or parasitic infections; hormonal disorders; metabolic  
 CC disorders; neurological disorders; gastrointestinal disorders; transport  
 CC disorders; and connective tissue disorders. They may also be used to  
 CC screen for modulators of protein activity or gene expression. DITHP  
 CC proteins can additionally be used in analysis of the proteome of a tissue  
 CC or cell type and to induce antibodies. The dithp nucleic acids are  
 CC additionally useful in somatic or germline gene therapy of the disorders  
 CC mentioned above, as a source of antisense sequences, as a source of  
 CC probes and primers, in genotyping and identification of individuals, in  
 CC the generation of transgenic animal models of human disease or knock in  
 CC humanised animals, in toxicological testing, and in transcript imaging.  
 CC The present sequence represents a DITHP protein which is an organelle-  
 CC associated protein.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 429 AA;  
 Query Match 91.9%; Score 1418; DB 24; Length 429;  
 Best Local Similarity 95.2%; Pred. No. 2e-143;  
 Matches 277; Conservative 3; Mismatches 5; Indels 6; Gaps 2;  
 QY 1 MTEQAISFAKDFLAGIAAIAISKTAVPIERVKLLQVQHASKQIADKQYGVDCIVR 60  
 DB 26 MTEQAISFAKDFLAGIAAIAISKTAVPIERVKLLQVQHASKQIADKQYGVDCIVR 85  
 QY 61 IPKEQGVLSFWRGNLANVIRFPQALNFAFDKTKQIFLGVDKHTQFWRFAGNLASG 120  
 DB 86 IPKEQGVLSFWRGNLANVIRFPQALNFAFDKTKQIFLGVDKHTQFWRFAGNLASG 145  
 QY 121 GAAAGTSLCFYVPLDPFARTRLAADVSGTEREERGLGDCIVKTKSGIRGLYQGFVS 180  
 DB 146 GAAAGTSLCFYVPLDPFARTRLAADVSGTEREERGLGDCIVKTKSGIRGLYQGFVS 205  
 QY 181 VOGIIITRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQTVTAAGVSYPPDVTARRMM 240  
 DB 206 VOGIIITRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQTVTAAGVSYPPDVTARRMM 265

QY 241 QSGRKGADIMYTGVDWCWRIKIFDEGKAFKGA-W-----SNVLRGNGKA 285  
 Db 266 QSGRKGADIMYTGVDWCWRIKIFDEGKAFKGA-FKGSNWKATLADALEGSPSA 316

## RESULT 11

AAW61169 standard; Protein: 298 AA.

AC AAW61169;

DT 28-SEP-1998 (first entry)

XX Ant1 protein.

XX Ant1; Adenine nucleotide translocator; cloning, screening;  
 KW DNA Tag dideoxy terminator cycle sequencing; oxidative phosphorylation;  
 KW probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;  
 KW hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;  
 KW lactic acidosis; degenerative muscle disease.

XX Mus gp.

XX WO9819714-A1.

XX PD -14-MAY-1998.

XX PF 31-OCT-1997; 97WO-US19882.

XX PR 01-NOV-1996; 96US-0030017.

XX (UYEM-) UNIV EMORY.

XX PI Graham BC, Macgregor GR, Wallace DC;

XX WPI; 1998-286608/25.

XX DR N-PSDB; AAV36479.

XX PT Mice lacking heart-muscle adenine nucleotide translocator protein -

XX PT useful as model for mitochondrial myopathy and hypertrophic

XX PT cardiomyopathy in animals and to test therapeutic compositions or

XX PT gene therapies

XX PS Disclosure; Page 39-40; 61pp; English.

XX CC The present sequence is the mouse Ant1 protein, the cDNA producing this  
 CC polypeptide is cloned by screening a mouse heart cDNA library with the  
 CC human Ant1 cDNA as a probe. The Ant1 cDNA sequence was determined by DNA  
 CC Tag dideoxy terminator cycle sequencing. The Ant1 protein is encoded by  
 CC the Ant1 locus, a nuclear gene on chromosome 8. This protein is required  
 CC in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP  
 CC which can then be converted into ATP. An Ant1 homozygous mutant would  
 CC thus be defective in OXPHOS which results in disease in oxidative  
 CC metabolism dependent tissues. This mouse Ant1 homozygous mutant can be  
 CC used as a model system for fascioscapular humeral muscular dystrophy,  
 CC hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model  
 CC systems can be used to test possible therapeutic compounds which  
 CC increase/mediate ATP and ADP exchange across the mitochondrial membrane  
 CC independent of Ant1.

XX SQ Sequence 298 AA;

Query Match 91.5%; Score 1412; DB 19; Length 298;

Best Local Similarity 88.6%; Pred. No. 5.4e-143; Mismatches 15; Indels 0; Gaps 0;

Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEQAIISFADFLAGGIAAISKTAAPIRRVKLLQVQHASKOIAADKQYKGIIVDCIVR 60

Db 1 MGQALSFLLDPLAGGIAAIVSKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVVR 60

QY 61 IPKEGQYLSFWRGKLANVIRYFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLAGS 120

Db 61 IPKEGQYLSFWRGKLANVIRYFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLAGS 120

QY 121 GAAGATSLCEVYPLDFARTRLAADVGKSGTEREERGLDCLVTKTSDDGIRGLYQGFSSVS 180

Db 121 GAAGATSLCEVYPLDFARTRLAADVGKSSQREFRNGDGLTKTKFKSDGLKGLYQGFSSVS 180

QY 181 VGGIIYRAAYFGVYDTAKMLPDPKXTHIVSMMIAQYTVAVAGVSYFPDTRRRMM 240

Db 181 VGGIIYRAAYFGVYDTAKMLPDPKXTHIVSMMIAQYTVAVAGVSYFPDTRRRMM 240

QY 241 QSGRKGADIMYTGVDWCWRIKIFDEGKAFKGA-SNVLRGNGKA-FVLVLYDELKKVI 298

Db 241 QSGRKGADIMYTGVDWCWRIKIFDEGKAFKGA-SNVLRGNGKA-FVLVLYDELKKVI 298

## RESULT 12

ABU53219 standard; Protein: 293 AA.

AC ABU53219;

DT 14-APR-2003 (first entry)

XX Human metabolism-associated DKFzphes3\_35n12 homologue #1.

XX Human; gene therapy; vaccine; disease treatment; detection.

XX Homo sapiens.

XX WO200112659-A2.

XX PD 22-FEB-2001.

XX PF 18-AUG-2000; 2000WO-IB01496.

XX PR 18-AUG-1999; 99US-0149499.

XX PR 28-SEP-1999; 99US-0156503.

XX (GEHU-) GERMAN HUMAN GENOME PROJECT.

XX PI Wiemann S;

XX WPI; 2001-327840/34.

XX PT Nucleic acids having the sequences of clones isolated from libraries of

XX PT different human tissues, useful in recombinant DNA methodologies -

XX PS Example III; Page 850; 1095pp; English.

XX CC This invention describes novel polynucleotides and polypeptides isolated  
 CC from human cDNA libraries which can be used for gene therapy or in  
 CC vaccines. The polynucleotides of the invention and antibodies encoded by  
 CC them may be used in the prevention, diagnosis and treatment of diseases  
 CC associated with inappropriate polypeptide expression. The products of the  
 CC invention may also be used to identify modulators of expression and  
 CC activity and to down regulate expression and activity. The antibodies of  
 CC the invention may also be used as diagnostic agents for detecting the  
 CC presence of polypeptides in samples. This sequence represents a homologue  
 CC of a polypeptide described in the disclosure of the invention.

XX SQ Sequence 293 AA;

Query Match 91.1%; Score 1406; DB 22; Length 293;

Best Local Similarity 90.1%; Pred. No. 2.3e-142; Mismatches 12; Indels 0; Gaps 0;

Matches 263; Conservative 17; Mismatches 12; Indels 0; Gaps 0;

QY 5 AISFADFLAGGIAAISKTAAPIRRVKLLQVQHASKOIAADKQYKGIIVDCIVR 64

Db 1 AISFADFLAGGIAAIVSKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVVR 60

QY 65 QGVLFWRGKLANVIRYFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLAGS 124

Db 61 QGVLFWRGKLANVIRYFPQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLAGS 120

QY 125 ATSLCFVPLDPFARTLADVKGSGTEREFRGLGDCLVKTKSGDGRGLYQGFVSVOGI 184  
DB 121 ATSLCFVPLDPFARTLADVKGSGTEREFRGLGDCLVKTKSGDGRGLYQGFVSVOGI 180  
QY 185 IIVRAAAGVVDYAKGMLPDPKXTHIVSWMIAQVTAVAGVSVPEPTVRRMMQSGR 244  
DB 181 IIVRAAAGVVDYAKGMLPDPKXTHIVSWMIAQVTAVAGVSVPEPTVRRMMQSGR 240  
QY 245 KGADIMVTGVDGKWKIFRDEGKAFKFGAMSNVLRGNGAFVLYLDELKX 296  
DB 241 KGADIMVTGVDGKWKIFRDEGKAFKFGAMSNVLRGNGAFVLYLDELKX 292

RESULT 13

AA71031  
ID AA71031 standard; Protein: 297 AA.  
XX  
AC AA71031;  
DT 29-AUG-2000 (first entry)  
XX  
DE Human adenine nucleotide translocator ANTL1.  
XX  
XX Human; adenine nucleotide translocator; ANTL1; mitochondria; ADP; ATP;  
KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;  
KW mitochondrial permeability transition; neuroprotective; neurologic;  
KW antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;  
KW antiparkinsonian; cerebroprotective; therapeutic; screening; psoriasis;  
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;  
KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;  
KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;  
KW mitochondrial diabetes and deafness; hyperproliferative disorder;  
KW myoclonic epilepsy red ragged fibre syndrome.

XX Homo sapiens.  
OS  
XX MO200026370-A2.  
XX  
XX 11-MAY-2000.  
XX  
XX 03-NOV-1999; 99WO-US25883.  
XX  
XX 03-NOV-1999; 98US-0185904.  
PR 08-SEP-1999; 99US-0393441.  
XX  
XX (MITO-) MITOKOR.  
XX  
XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;  
PI Ghosh SS;  
XX  
XX WPI: 2000-365619/31.  
DR N-PSDB; AAD00519.  
XX  
XX Recombinant construct encoding adenine nucleotide translocator  
PT polypeptide, useful e.g. in screening for potential therapeutic agents  
PT against mitochondrial disease  
XX  
XX Claim 44; Page 172; 175pp; English.

XX The patent discloses a method to produce adenine nucleotide translocator  
CC (ANT) proteins or ANT fusion proteins using recombinant expression  
CC constructs. ANT is a nuclear encoded protein and a major component of  
CC inner mitochondrial membrane. It mediates transport of adenosine  
CC di/tri-phosphates across the mitochondrial inner membrane and also serves  
CC as an important molecular component of the mitochondrial permeability  
CC transition pore, a modulator of apoptosis. ANT is used to identify agents  
CC or ligands that bind to, or interact with it. The ANT ligands are used to  
CC detect or isolate ANT in a biological sample, and therapeutically for  
CC regulating mitochondrial pore activity, for treating diseases associated  
CC with altered mitochondrial function, including Alzheimer's, Parkinson's  
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,  
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial  
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative

CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic  
CC epilepsy red ragged fibre syndrome. The present sequence is an  
CC adenine nucleotide translocator ANTL1 from human brain.  
XX  
SQ Sequence 297 AA;

Query Match 89.8%; Score 1385.5; DB 21; Length 297;  
Best Local Similarity 87.2%; Pred. No. 3.8e-140;  
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEGATSPADFLAGGIAAISTKAVPIERVKLLLOVQHASKOIADKQKIVDCIVR 60  
DB 1 MGDHAWFLDPLFAGAAVAAVSKTAVPIRVRKLLLOVQHASKOISAEKQKGIIDCVR 60  
QY 1PKEQGLSPFRGNLAVIRFPPTQALNPAFKDKYKQIFLGGVDKHPFRYFAGNLASG 120  
DB 61 IPEQGLSPFRGNLAVIRFPPTQALNPAFKDKYKQIFLGGVDKHPFRYFAGNLASG 120  
QY 121 GAAGATSLCFVPLDPFARTLADVKGSGTEREFRGLGDCLVKTKSGDGRGLYQGFVS 180  
DB 121 GAAGATSLCFVPLDPFARTLADVKGRR-AQREFRHGLGDCIIRKFKSDGRGLYQGFVS 179  
QY 181 VGGIIVRAAAGVVDYAKGMLPDPKXTHIVSWMIAQVTAVAGVSVPEPTVRRMM 240  
DB 180 VGGIIVRAAAGVVDYAKGMLPDPKXTHIVSWMIAQVTAVAGVSVPEPTVRRMM 239  
QY 241 QSGRGKADIMVTGVDGKWKIFRDEGKAFKFGAMSNVLRGNGAFVLYLDELKX 298  
DB 240 QSGRGKADIMVTGVDGKWKIFRDEGKAFKFGAMSNVLRGNGAFVLYLDELKX 297

RESULT 14

AAU0198  
ID AAU0198 standard; Protein: 297 AA.  
XX  
XX AAU0198;  
XX  
XX 07-SEP-2001 (first entry)  
XX  
XX Human adenine nucleotide translocator-1 (ANT-1) protein.  
XX  
XX Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;  
KW mitochondrial permeability transition pore component; cell survival;  
KW mitochondrial core component; mitochondrial related disorder; cancer;  
KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.  
XX  
XX Homo sapiens.  
OS  
XX MO200132876-A2.  
XX  
XX 10-MAY-2001.  
XX  
XX 03-NOV-2000; 2000WO-US30535.  
XX  
XX 03-NOV-1999; 99US-0434354.  
XX  
XX (MITO-) MITOKOR.

XX Murphy AN, Clevenger W, Wiley SE, Andreyev AV, Frigeri LG;  
PI Velicelbi G, Davis RE;  
XX  
XX WPI: 2001-291054/30.  
DR N-PSDB; AAS05901.  
XX

XX New nucleic acid expression constructs, useful for screening for agents  
PT that alter mitochondrial permeability transition (MPT), comprises  
PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide  
PT fused to energy transfer molecule

XX Disclosure; Fig 2; 186pp; English.  
XX  
XX The present sequence represents human adenine nucleotide translocator-1  
CC (ANT-1) protein. ANT proteins are mitochondrial permeability



CC transition (MTP) pore components responsible for mediating transport  
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact  
 CC with other mitochondrial core components e.g. cytochromes to  
 CC regulate MPT. The present invention relates to a novel nucleic acid  
 CC expression construct comprising a promoter operably linked to a  
 CC polynucleotide encoding a mitochondrial pore component polypeptide  
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein  
 CC (e.g. green fluorescent protein (GFP) or a FLAISH sequence). The novel  
 CC expression construct can alter mitochondrial membrane permeability  
 CC transition and/or alter the interaction between mitochondrial core  
 CC components. The methods are useful for screening for agents that alter  
 CC MPT and/or cell survival. These agents are useful for the prevention or  
 CC treatment of diseases associated with altered mitochondrial function or  
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes  
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,  
 CC mitochondrial encephalopathy, lactic acidosis, stroke,  
 CC hyperproliferative disorders e.g. cancer, and deafness.

CC Sequence 297 AA;

Query Match 89.8%; Score 1385.5; DB 22; Length 297;

Best Local Similarity 87.2%; Pred. No. 3.8e-140; Indels 1; Gaps 1;  
 Matches 260; Conservative 21; Mismatches 16;

QY 1 MTEQATSPADKFLAGIAAISTKTAVALPIERVKLLQVHASKOIAADKQYKGIIVDCIVR 60  
 DB 1 MGDHAWFLKDFLAGAVALAAVSKTAVAPIERVKLLQVHASKOISAEKQYKGIIVDCIVR 60  
 QY 61 IPKEQGLTSPWNRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVDRKHQFWRYPAGNLASG 120  
 DB 61 IPKEQGLTSPWNRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVDRKHQFWRYPAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDPARTRLAADVGKSTGEREFGIDGLKITKSDGIRGLYQGFVS 180  
 DB 121 GAAGATSLCFVYPLDPARTRLAADVGKRAQREHFGIDGLKITKSDGIRGLYQGFVS 179  
 QY 181 VGGIITRYRAAYFGVYDTAKGMLPDPKNTHTVSNMTAQVTAVAGVSYEPDVRRRMM 240  
 DB 180 VGGIITRYRAAYFGVYDTAKGMLPDPKNTHTVSNMTAQVTAVAGVSYEPDVRRRMM 239  
 QY 241 QSGRKADIMYTGVDWCWKIFPDEGGAFFKAGMSNVLRMGCAFVLVYDELKRYI 298  
 DB 240 QSGRKADIMYTGVDWCWKIKADDEGAKAFKAGMSNVLRMGCAFVLVYDELKRYI 297

RESULT 15

AAU10378 standard; Protein; 297 AA.

AC AAU10378;

DT 14-FEB-2002 (first entry)

DE Human adenine nucleotide translocator 1 (ANT1).

KM Human; adenine nucleotide translocator; ANT;

KM mitochondrial matrix protein.

OS Homo sapiens.

PN WO200185944-A2.

PD 15-NOV-2001.

PF 11-MAY-2001; 2001WO-US15416.

PR 11-MAY-2000; 2000US-0569327.

PA (MITO-) MITOKOR.

PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;  
 PI Ghosh SS, Moos WH, Pei Y, Carroll AK;

DR WPI; 2002-055598/07.  
 DR N-PSDB; AAS16688.

PT Novel recombinant expression construct for producing adenine nucleotide

PT translocator polypeptides, comprises a regulated promoter linked to

PS nucleic acid encoding the polypeptide

PS Claim 44; Fig 2; 147pp; English.

CC The invention relates to a recombinant expression construct (1)  
 CC comprising a regulated promoter operably linked to a nucleic acid  
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT  
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial  
 CC matrix for ADP in the cytosol. (1) is useful for producing recombinant  
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and  
 CC culturing the host cell. (1) is also useful for targeting a polypeptide  
 CC of interest to a mitochondrial membrane, where ANT polypeptide is  
 CC expressed as a fusion protein with the polypeptide of interest.  
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is  
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT  
 CC ligand is useful for determining the presence of an ANT polypeptide,  
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating  
 CC ANT from a biological sample, where the ANT ligand is covalently or non-  
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also  
 CC useful for identifying an agent that interacts with an ANT polypeptide.  
 CC The present sequence represents the amino acid sequence of human ANT1.

CC Sequence 297 AA;

Query Match 89.8%; Score 1385.5; DB 23; Length 297;

Best Local Similarity 87.2%; Pred. No. 3.8e-140; Indels 1; Gaps 1;  
 Matches 260; Conservative 21; Mismatches 16;

QY 1 MTEQATSPADKFLAGIAAISTKTAVALPIERVKLLQVHASKOIAADKQYKGIIVDCIVR 60  
 DB 1 MGDHAWFLKDFLAGAVALAAVSKTAVAPIERVKLLQVHASKOISAEKQYKGIIVDCIVR 60  
 QY 61 IPKEQGLTSPWNRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVDRKHQFWRYPAGNLASG 120  
 DB 61 IPKEQGLTSPWNRGNLANVIRYPTQALNFAFKDKYKQIFLGVDVDRKHQFWRYPAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDPARTRLAADVGKSTGEREFGIDGLKITKSDGIRGLYQGFVS 180  
 DB 121 GAAGATSLCFVYPLDPARTRLAADVGKRAQREHFGIDGLKITKSDGIRGLYQGFVS 179  
 QY 181 VGGIITRYRAAYFGVYDTAKGMLPDPKNTHTVSNMTAQVTAVAGVSYEPDVRRRMM 240  
 DB 180 VGGIITRYRAAYFGVYDTAKGMLPDPKNTHTVSNMTAQVTAVAGVSYEPDVRRRMM 239  
 QY 241 QSGRKADIMYTGVDWCWKIFPDEGGAFFKAGMSNVLRMGCAFVLVYDELKRYI 298  
 DB 240 QSGRKADIMYTGVDWCWKIKADDEGAKAFKAGMSNVLRMGCAFVLVYDELKRYI 297

Search completed: December 18, 2003, 17:10:50  
 Job time : 43 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 18, 2003, 17:07:54 ; Search time 17 Seconds  
(without alignments)  
824.350 Million cell updates/sec

Title: US-09-185-904A-33

Sequence: 1 MTEQALISPAKFLAGGIAA.....LRMGARVLYVDELKVTI 298

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Swissprot\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1543	100.0	298	ADT3_HUMAN	P12236 homo sapien
2	1512	98.0	298	ADT3_BOVIN	P32007 bos tauru
3	1463	94.8	298	ADT2_HUMAN	P05141 homo sapien
4	1451	94.0	298	ADT2_RAT	Q09773 rattus norv
5	1445	93.6	298	ADT2_MOUSE	P51881 mus musculu
6	1424	92.3	298	ADT1_RAT	Q05962 rattus norv
7	1418	91.9	298	ADT1_MOUSE	P48962 mus musculu
8	1417	91.8	297	ADT1_BOVIN	P02722 bos tauru
9	1409	91.3	298	ADT1_HUMAN	P12235 homo sapien
10	1254.5	81.3	299	ADT1_MOUSE	Q26365 drosophila
11	1204	78.0	301	ADT1_MOUSE	Q27238 anopheles g
12	978	63.4	339	ADT1_MOUSE	P31692 chlorella k
13	778.5	50.5	307	ADT3_YEAST	P18338 saccharomyc
14	772	50.0	308	ADT1_MOUSE	P27080 chlamydomon
15	769	49.8	322	ADT1_MOUSE	Q09188 schistosom
16	768	49.8	322	ADT1_MOUSE	Q22242 goseypium h
17	766	49.6	313	ADT1_MOUSE	P02723 neuropeptid
18	762.5	49.4	305	ADT1_MOUSE	P49382 kluyveromyc
19	760.5	49.3	318	ADT2_YEAST	P18339 saccharomyc
20	750.5	48.6	385	ADT1_MOUSE	P40341 arabidopsis
21	750	48.6	387	ADT1_MOUSE	P40409 zea mays (m
22	748	48.5	386	ADT1_MOUSE	P25083 solanum tub
23	747	48.4	382	ADT1_MOUSE	P31891 oryza sativ
24	744	48.2	387	ADT1_MOUSE	P12857 zea mays (m
25	742.5	48.1	381	ADT1_MOUSE	P31167 arabidopsis
26	740	48.0	331	ADT1_MOUSE	Q41629 tritlicum ae
27	739.5	47.9	386	ADT2_MOUSE	P27081 solanum tub
28	737.5	47.8	309	ADT1_MOUSE	P04710 saccharomyc
29	727	47.1	331	ADT2_MOUSE	Q41630 tritlicum ae
30	305.5	19.8	565	CMC3_CABEL	Q19529 caenorhabdi
31	302	19.6	588	CMC2_CABEL	Q20799 caenorhabdi
32	300	19.4	330	GDC_BOVIN	Q01888 bos tauru
33	299	19.4	307	ODC2_YEAST	Q09297 saccharomyc

34	295	19.1	678	1	CMC1_HUMAN	Q75746 homo sapien
35	289.5	18.8	322	1	GDC_RAT	P12631 rattus norv
36	287.5	18.6	702	1	CMC1_CABEL	Q21153 caenorhabdi
37	286	18.5	325	1	UCP5_HUMAN	Q95258 homo sapien
38	285	18.5	332	1	GDC_HUMAN	P16260 homo sapien
39	284	18.4	325	1	UCP5_MOUSE	Q92282 mus musculu
40	282.5	18.3	326	1	YB08_SCHPO	Q13805 echinosacch
41	280	18.1	675	1	CMC2_HUMAN	Q91800 homo sapien
42	272	17.6	315	1	MFT_HUMAN	Q91241 homo sapien
43	270	17.5	315	1	SA18_HUMAN	Q91144 homo sapien
44	265	17.2	312	1	UCP3_HUMAN	P55916 homo sapien
45	265	17.2	676	1	CMC2_MOUSE	Q99x4 mus musculu

## ALIGNMENTS

RESULT 1  
ADT3\_HUMAN STANDARD; PRT; 298 AA.  
AC P12236; Q96C49;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE ADP/ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)  
DE (Mentine nucleotide translocator 3) (ANT 3).  
DE SLIC25A6 OR ANT3.  
GN Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Metazoa; Primates; Carnivora; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89236396; PubMed=2541251;  
RA Cozens A.L., Runswick M.J., Walker J.E.;  
RT "DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase.";  
RL J. Mol. Biol. 206:261-280(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Zhou J., Yu W., Tang H., Tsang Y.T.M., Bouck J., Gibbs R.A., Margolin J.F.;  
RN Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain, Cervix, Eye, and Lung;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Heide F., Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L., Stempleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C., Roark S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bask S.A., McManis P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W., Viallton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heltan E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E., Schnerker A., Schein J.B., Jones S.J.W., Matra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [4]  
RP SEQUENCE OF 36-298 FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=88124845; PubMed=2829183;  
RA Houldsworth J., Attardi G.;  
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA

**THIS PAGE BLANK (USPTO)**

level 1 adult human liver." ;  
Proc Natl Acad Sci U S A. 85:377-381(1988).  
CC CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
MITOCHONDRIAL INNER MEMBRANE.  
CC CC -1- SUBUNIT: Homodimer.  
CC CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
inner membrane.  
CC CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
CC CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation  
at the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement ([see http://www.isb-sib.ch/announce/](http://www.isb-sib.ch/announce/)  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
DR EMBL; J03592; AAA36750.1; -;  
DR EMBL; AY007135; AAG01988.1; -;  
DR EMBL; BC007295; AAH07295.1; -;  
DR EMBL; BC007850; AAH07850.1; -;  
DR EMBL; BC008737; AAH08737.1; -;  
DR EMBL; BC008935; AAH08935.1; -;  
DR EMBL; BC014775; AAH14775.1; -;  
DR PIR; S03894; S03894. -;  
DR Genew; HGNC:10992; SLIC25A6.  
DR MIM; 300151; -;  
DR GO; GO:0005474; C:mitochondrial inner membrane translocase co. . ; TAS.  
DR GO; GO:0005571; F:ATP/ADP antiporter activity; NAS.  
DR GO; GO:0006854; P:ATP/ADP exchange; TAS.  
DR InterPro; IPR002067; Mlt\_carrier.  
DR InterPro; IPR002030; Mlt\_uncoupling.  
DR InterPro; IPR001993; Mitoch\_carrier.  
DR Pfam; PF00153; mltc\_carr; 3  
DR PRINTS; PR00926; MITOCARRIER.  
DR PROSITE; PS00784; MTUNCOUPLING.  
DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
KW Mitochondonction; Inner membrane; Repeat; Transmembrane; Transport;  
MultiGene family.  
FT TRANSMEM 12 29 1 (POTENTIAL).  
FT TRANSMEM 73 91 2 (POTENTIAL).  
FT TRANSMEM 117 134 3 (POTENTIAL).  
FT TRANSMEM 176 195 4 (POTENTIAL).  
FT TRANSMEM 214 231 5 (POTENTIAL).  
FT TRANSMEM 273 291 6 (POTENTIAL).  
FT REPEAT 1 100 1.  
FT REPEAT 101 208 2.  
FT REPEAT 209 298 3.  
FT CONFLICT 105 108 KHTQ -> RHA (IN REF. 4).  
FT CONFLICT 242 242 S -> F (IN REF. 3; AAH14775).  
SQ SEQUENCE 298 AA; 32866 MW; 18534EBF0E49672F CRC64;

QY	DB	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
QY	DB	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
QY	DB	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
QY	DB	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
QY	DB	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
QY	DB	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
QY	DB	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
QY	DB	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
QY	DB	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
QY	DB	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29																															

**THIS PAGE BLANK (USPTO)**

61 IPKQGVLSFWRGNLANVIRYPTOLNFAFDKRYKOIFLGVDKHTOFWRYPAGNLAG 120  
 Db 61 IPKQGVLSFWRGNLANVIRYPTOLNFAFDKRYKOIFLGVDKHTOFWRYPAGNLAG 120  
 Qy 121 GAAGATSLCFVYPPLDFAFRLADVGKSTEREFRGLGDCVKTITKSDIRGLYOGFSVS 180  
 Db 121 GAAGATSLCFVYPPLDFAFRLADVGKSTEREFRGLGDCVKTITKSDIRGLYOGFSVS 180  
 Qy 181 VOGIITVAAVFGVYDPAKGMPLDPKNTIIVSWIAQTVTAAGVSVYPTVARRMM 240  
 Db 181 VOGIITVAAVFGVYDPAKGMPLDPKNTIIVSWIAQTVTAAGVSVYPTVARRMM 240  
 Qy 241 QSGRGADIMVTGTVDCWRKIFRDEGGAFFKGAWSNVLKMGAFVLYVDELKVI 298  
 Db 241 QSGRGADIMVTGTVDCWRKIFRDEGGAFFKGAWSNVLKMGAFVLYVDELKVI 298

RESULT 3  
 A.T2 HUMAN  
 1.0 ADT2 HUMAN STANDARD; PRT; 298 AA.  
 AC POS141; Q43350; (Rel. 05, Created)  
 EF 13-AUG-1987 (Rel. 05, Last sequence update)  
 EF 01-OCT-1994 (Rel. 30, Last sequence update)  
 EF 28-FEB-2003 (Rel. 41, Last annotation update)  
 D3 ADP carrier protein, fibroblast isoform (ADP/ATP translocase 2)  
 D3 (Adenine nucleotide translocator 2) (ANT 2).  
 GN SLIC25A5 OR ANT2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=90375457; PubMed=2168878;  
 RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Muzel J.;  
 RT "The human fibroblast adenine nucleotide translocator gene. Molecular  
 cloning and sequence."  
 RL J. Biol. Chem. 265:16060-16063 (1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=87166056; PubMed=3031073;  
 RA Battini R., Ferrarri S., Kaczmarek L., Calabretta B., Chen S.T.,  
 RA Baserga R.;  
 RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is  
 growth-regulated."  
 RL J. Biol. Chem. 262:4355-4358 (1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=87166056; PubMed=3031073;  
 RA Mazzarella R.A., Schlesinger D., Chen E.Y.;  
 RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=87166056; PubMed=3031073;  
 RA Becker M., Graves T., Ozerky P.;  
 RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 47-298 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=88124845; PubMed=2829183;  
 RA Houldsworth J., Attardi G.;  
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA  
 level in adult human liver."  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381 (1988).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC at the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

DR EMBL; M57424; AAA51737.1; -  
 DR EMBL; J02683; AAA35579.1; -  
 DR EMBL; L78810; AAB39266.1; -  
 DR EMBL; AC004000; AAB96347.1; -  
 DR EMBL; J03591; AAA6749.1; -  
 DR PIR; A29132; A29132.  
 DR Genew; HGNC:10991; SLIC25A5.  
 DR MIM; 300150; -  
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.  
 DR GO; GO:0015207; F: adenine transporter activity; TAS.  
 DR GO; GO:0006832; P: small molecule transport; TAS.  
 DR InterPro; IPR002067; Mlt\_carrier.  
 DR InterPro; IPR002030; Mlt\_carrier.  
 DR Pfam; PF00153; mito\_carr; 3  
 DR PRINTS; PR00926; MITOCARRIER.  
 DR PRINTS; PR00784; MITOCARRIER.  
 DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 KW Multigene family.  
 FT TRANSMEM 12 29  
 FT TRANSMEM 73 91  
 FT TRANSMEM 117 134  
 FT TRANSMEM 176 195  
 FT TRANSMEM 214 231  
 FT TRANSMEM 273 291  
 FT REPEAT 1 111  
 FT REPEAT 112 208  
 FT REPEAT 209 298  
 FT CONFLICT 6 6 V -> L (IN REF. 2).  
 FT CONFLICT 66 66 G -> E (IN REF. 2).  
 FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).  
 FT CONFLICT 162 162 V -> G (IN REF. 5).  
 SQ SEQUENCE 298 AA; 32895 MW; F973C3AED92C49D3 CRC64;

Query Match 94.8%; Score 1463; DB 1; Length 298;  
 Best Local Similarity 92.9%; Pred. No. 3; 8e-121;  
 Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MTEOASFANDFLAGGIAAISTAVAPIERVYLLQVHASKQIAADKQYKGIIVCTVR 60  
 Db 1 MTEOASFANDFLAGGIAAISTAVAPIERVYLLQVHASKQIAADKQYKGIIVCTVR 60  
 Qy 61 IPKQGVLSFWRGNLANVIRYPTOLNFAFDKRYKOIFLGVDKHTOFWRYPAGNLAG 120  
 Db 61 IPKQGVLSFWRGNLANVIRYPTOLNFAFDKRYKOIFLGVDKHTOFWRYPAGNLAG 120  
 Qy 121 GAAGATSLCFVYPPLDFAFRLADVGKSTEREFRGLGDCVKTITKSDIRGLYOGFSVS 180  
 Db 121 GAAGATSLCFVYPPLDFAFRLADVGKSTEREFRGLGDCVKTITKSDIRGLYOGFSVS 180  
 Qy 181 VOGIITVAAVFGVYDPAKGMPLDPKNTIIVSWIAQTVTAAGVSVYPTVARRMM 240  
 Db 181 VOGIITVAAVFGVYDPAKGMPLDPKNTIIVSWIAQTVTAAGVSVYPTVARRMM 240  
 Qy 241 QSGRGADIMVTGTVDCWRKIFRDEGGAFFKGAWSNVLKMGAFVLYVDELKVI 298  
 Db 241 QSGRGADIMVTGTVDCWRKIFRDEGGAFFKGAWSNVLKMGAFVLYVDELKVI 298

RESULT 4  
 ADT2 RAT  
 ID ADT2 RAT STANDARD; PRT; 298 AA.  
 AC Q09073;  
 DT 01-FEB-1995 (Rel. 31, Created)

**THIS PAGE BLANK (USPTO)**